



SEQUENCE LISTING

<110> Smith, Leonard A.
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Brown, Douglas R.

<120> RECOMBINANT VACCINE AGAINST BOTULINUM
NEUROTOXIN

<130> A33626 067252.0105

<140> 09/611,419

<141> 2000-07-06

<150> PCT/US00/12890

<151> 2000-05-12

<150> 60/133,865

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<150> 60/133,866

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<150> 60/146,192

<151> 1999-07-29

<150> 08/123,975

<151> 1993-09-21

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<210> 1

<211> 1332

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTA Hc

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acctccatcc tgaacctgcg ctacgaatcc aatcacctga tcgacctgtc tcgctacgct 120
tccaaaatca acatcggttc taaagttaac ttcgatccga tcgacaagaa tcagatccag 180

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ctgttcaatc tggaaatcttc caaaatcgaa gttatcctga agaatgctat cgtataacaac 240
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atctctctga acaatgaata caccatcatc aactgcatgg aaaacaattc tgggttgaaa 360
gtatctctga actacgggtga aatcatctgg actctgcagg acactcagga aatcaaacag 420
cgtgttgtat tcaaatactc tcagatgata aacatctctg actacatcaa tcgctggatc 480
ttcgttacca tcaccaacaa tcgtctgaat aactccaaaa tctacatcaa cggccgtctg 540
atcgaccaga aaccgatctc caatctgggt aacatccacg cttctaataa catcatgttc 600
aaactggacg gttgtcgtga cactcacgcg tacatctgga tcaaatactt caatctgttc 660
gacaaagaac tgaacgaaaa agaaatcaaa gacctgtacg acaaccagtc caattctggg 720
atcctgaaag acttctgggg tgactacctg cagtacgaca aaccgtacta catgctgaat 780
ctgtacgata cgaacaaata cgttgacgct aacaatgtag gtatccgcgg ttacatgtac 840
ctgaaaggtc cgcgtgggtc tgttatgact accaactctt acctgaactc ttccctgtac 900
cgtgggtacca aattcatcat caagaaatac gcgtctggta acaaggacaa tatcgttcgc 960
aacaatgata gtgtatacat caatgttgta gttaagaaca aagaataccg tctgggtacc 1020
aatgcttctc aggtctgggt agaaaagata ttgtctgctc tggaaatccc ggacgttggg 1080
aatctgtctc aggtagttgt aatgaaatcc aagaacgacc agggtatcac taacaaatgc 1140
aaaatgaatc tgcaggacaa caatggtaac gatatcggtt tcatcggttt ccaccagttc 1200
aacaatatcg ctaaactggg tgcttccaac tgggtacaatc gtcagatcga acgttcctct 1260
cgcactctgg gttgctcttg ggagttcatc ccggttgatg acggttgggg tgaacgtccg 1320
ctgtaagaat tc 1332

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<210> 2

<211> 437

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTA Hc

<400> 2

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Met Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn
 1           5           10           15
Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
          20           25           30
Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
          35           40           45
Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
          50           55           60
Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
65           70           75           80
Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
          85           90           95
Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
          100          105          110
Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
          115          120          125
Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
          130          135          140
Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
145          150          155          160
Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
          165          170          175
Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
          180          185          190
Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
          195          200          205

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Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
 210 215 220
 Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
 225 230 235 240
 Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn
 245 250 255
 Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg
 260 265 270
 Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn
 275 280 285
 Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys
 290 295 300
 Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg
 305 310 315 320
 Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr
 325 330 335
 Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile
 340 345 350
 Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn
 355 360 365
 Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn
 370 375 380
 Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala
 385 390 395 400
 Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser
 405 410 415
 Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp
 420 425 430
 Gly Glu Arg Pro Leu
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<210> 3
 <211> 1323
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTA Hc

<400> 3
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 aacatcggtt ctaaagttaa cttcgatccg atcgacaaga atcagatcca gctgttcaat 180
 ctggaatctt ccaaaatcga agttatcctg aagaatgcta tcgtatacaa ctctatgtac 240
 gaaaacttct ccacctcctt ctggatccgt atcccgaat acttcaactc catctctctg 300
 aacaatgaat acaccatcat caactgcatg gaaaacaatt ctggttgga agtatctctg 360
 aactacggtg aaatcatctg gactctgcag gacactcagg aaatcaaaca gcgtgttgta 420
 ttcaaatact ctcagatgat caacatctct gactacatca atcgctggat cttcgttacc 480
 atcaccaaca atcgtctgaa taactccaaa atctacatca acggccgtct gatcgaccag 540
 aaaccgatct ccaatctggg taacatccac gcttctaata acatcatgtt caaactggac 600
 ggttgctcgtg aactcaccg ctacatctgg atcaaatact tcaatctggt cgacaaagaa 660
 ctgaacgaaa aagaaatcaa agacctgtac gacaaccagt ccaattctgg tatcctgaaa 720
 gacttctggg gtgactacct gcagtacgac aaaccgtact acatgctgaa tctgtacgat 780
 ccgaacaaat acgttgacgt caacaatgta ggtatccgcg gttacatgta cctgaaaggt 840
 ccgcgtgggt ctgttatgac taccaacatc tacctgaact cttccctgta ccgtgggtacc 900
 aaattcatca tcaagaaata cgcgtctggt aacaaggaca atatcgttcg caacaatgat 960

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cgtgtataca tcaatgttgt agttaagaac aaagaatacc gtctgggtac caatgcttct 1020
caggctgggtg tagaaaagat cttgtctgct ctggaaatcc cggacgttgg taatctgtct 1080
caggtagttg taatgaaatc caagaacgac cagggtatca ctaacaaatg caaatgaat 1140
ctgcaggaca acaatggtaa cgatatcggt ttcacggtt tccaccagtt caacaatatc 1200
gctaaactgg ttgcttccaa ctggtacaat cgtcagatcg aacgttcctc tcgcactctg 1260
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ttc 1323

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<210> 4

<211> 434

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTA Hc

<400> 4

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Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr
 20           25           30
Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp
 35           40           45
Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val
 50           55           60
Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser
 65           70           75           80
Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu
 85           90           95
Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp
 100          105          110
Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr
 115          120          125
Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn
 130          135          140
Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn
 145          150          155          160
Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln
 165          170          175
Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met
 180          185          190
Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys
 195          200          205
Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp
 210          215          220
Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly
 225          230          235          240
Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp
 245          250          255
Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met
 260          265          270
Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu
 275          280          285
Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala
 290          295          300
Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile

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305		310		315		320
Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser						
	325		330		335	
Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val						
	340		345		350	
Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly						
	355		360		365	
Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp						
	370		375		380	
Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val						
385		390		395		400
Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu						
	405		410		415	
Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg						
	420		425		430	
Pro Leu						

<210> 5
 <211> 1326
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTA Hc

<400> 5
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 atcaacatcg gttctaaagt taacttcgat ccgatcgaca agaatcagat ccagctgttc 180
 aatctggaat cttccaaaat cgaagttatc ctgaagaatg ctatcgtata caactctatg 240
 tacgaaaact tctccacctc cttctggatc cgtatcccga aatacttcaa ctccatctct 300
 ctgaacaatg aatacaccat catcaactgc atggaaaaca attctgggtg gaaagtatct 360
 ctgaactacg gtgaaatcat ctggactctg caggacactc aggaaatcaa acagcgtggt 420
 gtattcaaat actctcagat gatcaacatc tctgactaca tcaatcgctg gatcttcggt 480
 accatcacca acaatcgtct gaataactcc aaaatctaca tcaacggccg tctgatcgac 540
 cagaaaccga tctccaatct gggtaacatc cacgcttcta ataacatcat gttcaaactg 600
 gacggttgct gtgacactca ccgctacatc tggatcaaat acttcaatct gttcgacaaa 660
 gaactgaacg aaaaagaaat caaagacctg tacgacaacc agtccaattc tggatatcctg 720
 aaagacttct ggggtgacta cctgcagtac gacaaaccgt actacatgct gaatctgtac 780
 gatccgaaca aatacgttga cgtcaacaat gtaggtatcc gcggttacat gtacctgaaa 840
 ggtccgcgtg gttctgttat gactaccaac atctacctga actcttccct gtaccgtggt 900
 accaaattca tcatcaagaa atacgcgtct ggtaacaagg acaatatcgt tcgcaacaat 960
 gatcgtgtat acatcaatgt tgtagttaag aacaaagaat accgtctggc taccaatgct 1020
 tctcaggctg gtgtagaaaa gatcttgtct gctctggaaa tcccggacgt tggtaatctg 1080
 tctcaggtag ttgtaatgaa atccaagaac gaccagggtg tctaatacaa atgcaaaatg 1140
 aatctgcagg acaacaatgg taacgatatc ggtttcatcg gtttccacca gttcaacaat 1200
 atcgctaaac tggttgcttc caactggtac aatcgtcaga tcgaacgttc ctctcgact 1260
 ctgggttgct cttgggagtt catcccggtt gatgacggtt ggggtgaacg tccgctgtaa 1320
 gaattc 1326

<210> 6
 <211> 435
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTA Hc

<400> 6

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Ile	Leu	Asn	Leu	Arg	Tyr	Glu	Ser	Asn	His	Leu	Ile	Asp	Leu	Ser	Arg
		20						25				30			
Tyr	Ala	Ser	Lys	Ile	Asn	Ile	Gly	Ser	Lys	Val	Asn	Phe	Asp	Pro	Ile
		35					40					45			
Asp	Lys	Asn	Gln	Ile	Gln	Leu	Phe	Asn	Leu	Glu	Ser	Ser	Lys	Ile	Glu
	50					55					60				
Val	Ile	Leu	Lys	Asn	Ala	Ile	Val	Tyr	Asn	Ser	Met	Tyr	Glu	Asn	Phe
65					70					75					80
Ser	Thr	Ser	Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Ser	Ile	Ser
			85						90					95	
Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Glu	Asn	Asn	Ser	Gly
			100						105				110		
Trp	Lys	Val	Ser	Leu	Asn	Tyr	Gly	Glu	Ile	Ile	Trp	Thr	Leu	Gln	Asp
		115					120					125			
Thr	Gln	Glu	Ile	Lys	Gln	Arg	Val	Val	Phe	Lys	Tyr	Ser	Gln	Met	Ile
	130					135					140				
Asn	Ile	Ser	Asp	Tyr	Ile	Asn	Arg	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn
145					150					155					160
Asn	Arg	Leu	Asn	Asn	Ser	Lys	Ile	Tyr	Ile	Asn	Gly	Arg	Leu	Ile	Asp
			165						170					175	
Gln	Lys	Pro	Ile	Ser	Asn	Leu	Gly	Asn	Ile	His	Ala	Ser	Asn	Asn	Ile
		180						185					190		
Met	Phe	Lys	Leu	Asp	Gly	Cys	Arg	Asp	Thr	His	Arg	Tyr	Ile	Trp	Ile
		195					200					205			
Lys	Tyr	Phe	Asn	Leu	Phe	Asp	Lys	Glu	Leu	Asn	Glu	Lys	Glu	Ile	Lys
	210					215					220				
Asp	Leu	Tyr	Asp	Asn	Gln	Ser	Asn	Ser	Gly	Ile	Leu	Lys	Asp	Phe	Trp
225					230					235					240
Gly	Asp	Tyr	Leu	Gln	Tyr	Asp	Lys	Pro	Tyr	Tyr	Met	Leu	Asn	Leu	Tyr
			245						250				255		
Asp	Pro	Asn	Lys	Tyr	Val	Asp	Val	Asn	Asn	Val	Gly	Ile	Arg	Gly	Tyr
		260					265					270			
Met	Tyr	Leu	Lys	Gly	Pro	Arg	Gly	Ser	Val	Met	Thr	Thr	Asn	Ile	Tyr
		275					280					285			
Leu	Asn	Ser	Ser	Leu	Tyr	Arg	Gly	Thr	Lys	Phe	Ile	Ile	Lys	Lys	Tyr
	290					295					300				
Ala	Ser	Gly	Asn	Lys	Asp	Asn	Ile	Val	Arg	Asn	Asn	Asp	Arg	Val	Tyr
305					310					315					320
Ile	Asn	Val	Val	Val	Lys	Asn	Lys	Glu	Tyr	Arg	Leu	Ala	Thr	Asn	Ala
			325						330					335	
Ser	Gln	Ala	Gly	Val	Glu	Lys	Ile	Leu	Ser	Ala	Leu	Glu	Ile	Pro	Asp
		340						345					350		
Val	Gly	Asn	Leu	Ser	Gln	Val	Val	Met	Lys	Ser	Lys	Asn	Asp	Gln	
		355					360					365			
Gly	Ile	Thr	Asn	Lys	Cys	Lys	Met	Asn	Leu	Gln	Asp	Asn	Asn	Gly	Asn
	370					375					380				
Asp	Ile	Gly	Phe	Ile	Gly	Phe	His	Gln	Phe	Asn	Asn	Ile	Ala	Lys	Leu
385					390					395					400
Val	Ala	Ser	Asn	Trp	Tyr	Asn	Arg	Gln	Ile	Glu	Arg	Ser	Ser	Arg	Thr
			405						410					415	

Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu
 420 425 430
 Arg Pro Leu
 435

<210> 7
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTB Hc

<400> 7
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 gacggtgttg aactgaatga caagaaccag ttcaaaactga cctcttccgc taactctaag 180
 atccgtgtta ctcagaatca gaacatcatc ttcaactccg tattcctgga cttctctgtt 240
 tcttcttgga ttctgatccc gaaatacaag aacgacggta tccagaatta catccacaat 300
 gaatacacca tcatcaactg catgaagaat aactctgggt ggaagatctc catccgcggg 360
 aaccgtatca tctggactct gatcgatatac aacggtaaga ccaaatctgt attcttcgaa 420
 tacaacatcc gtgaagacat ctctgaatac atcaatcgct gggtcttcgt taccatcacc 480
 aataacctga acaatgctaa aatctacatc aacggtaaac tggaatctaa taccgacatc 540
 aaagacatcc gtgaagttat cgctaaccgt gaaatcatct tcaaactgga cggtgacatc 600
 gatcgtaacc agttcatctg gatgaaatac ttctccatct tcaacaccga actgtctcag 660
 tccaatatcg aagaacggta caagatccag tcttactccg aataacctgaa agacttctgg 720
 ggtaatccgc tgatgtacaa caagaatac tatatgttca atgctggtaa caagaactct 780
 tacatcaaac tgaagaaaga ctctccgggt ggtgaaatcc tgactcggtc caaatacaac 840
 cagaactcta aatacatcaa ctaccgcgac ctgtacatcg gtgaaaagtt catcatccgt 900
 cgcaaactcta actctcagtc catcaatgat gacatcgta gtaaagaaga ctacatctac 960
 ctggacttct tcaacctgaa tcaggaatgg cgtgtataca cctacaagta cttcaagaaa 1020
 gaagaagaaa agcttttctt ggctccgata tctgattccg acgaactcta caacaccatc 1080
 cagatcaaag aatacgacga acagccgacc tactcttgcc agctgctggt caagaaagat 1140
 gaagaatcta ctgacgaaat cggctctgac ggtatccacc gtttctacga atctgggtatc 1200
 gtattcgaag aatacaaaga ctacttctgc atctccaaat ggtacctgaa ggaagttaa 1260
 cgcaaaccgt acaacctgaa actgggttgc aattggcagt tcatcccga agacgaaggt 1320
 tggaccgaat agtaagaatt c 1341

<210> 8
 <211> 440
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Encoded polypeptide of a synthetic construct based
 on BoNTB Hc

<400> 8
 Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn
 1 5 10 15
 Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala
 20 25 30
 Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn Gln Phe
 35 40 45
 Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln Asn Gln
 50 55 60

Asn	Ile	Ile	Phe	Asn	Ser	Val	Phe	Leu	Asp	Phe	Ser	Val	Ser	Phe	Trp
65				70					75					80	
Ile	Arg	Ile	Pro	Lys	Tyr	Lys	Asn	Asp	Gly	Ile	Gln	Asn	Tyr	Ile	His
			85					90						95	
Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Lys	Asn	Asn	Ser	Gly	Trp	Lys
			100					105					110		
Ile	Ser	Ile	Arg	Gly	Asn	Arg	Ile	Ile	Trp	Thr	Leu	Ile	Asp	Ile	Asn
			115				120					125			
Gly	Lys	Thr	Lys	Ser	Val	Phe	Phe	Glu	Tyr	Asn	Ile	Arg	Glu	Asp	Ile
			130			135					140				
Ser	Glu	Tyr	Ile	Asn	Arg	Trp	Phe	Phe	Val	Thr	Ile	Thr	Asn	Asn	Leu
145				150						155					160
Asn	Asn	Ala	Lys	Ile	Tyr	Ile	Asn	Gly	Lys	Leu	Glu	Ser	Asn	Thr	Asp
			165					170						175	
Ile	Lys	Asp	Ile	Arg	Glu	Val	Ile	Ala	Asn	Gly	Glu	Ile	Ile	Phe	Lys
			180					185						190	
Leu	Asp	Gly	Asp	Ile	Asp	Arg	Thr	Gln	Phe	Ile	Trp	Met	Lys	Tyr	Phe
			195				200					205			
Ser	Ile	Phe	Asn	Thr	Glu	Leu	Ser	Gln	Ser	Asn	Ile	Glu	Glu	Arg	Tyr
			210			215					220				
Lys	Ile	Gln	Ser	Tyr	Ser	Glu	Tyr	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Pro
225				230						235					240
Leu	Met	Tyr	Asn	Lys	Glu	Tyr	Tyr	Met	Phe	Asn	Ala	Gly	Asn	Lys	Asn
			245						250					255	
Ser	Tyr	Ile	Lys	Leu	Lys	Lys	Asp	Ser	Pro	Val	Gly	Glu	Ile	Leu	Thr
			260					265						270	
Arg	Ser	Lys	Tyr	Asn	Gln	Asn	Ser	Lys	Tyr	Ile	Asn	Tyr	Arg	Asp	Leu
			275				280					285			
Tyr	Ile	Gly	Glu	Lys	Phe	Ile	Ile	Arg	Arg	Lys	Ser	Asn	Ser	Gln	Ser
			290			295					300				
Ile	Asn	Asp	Asp	Ile	Val	Arg	Lys	Glu	Asp	Tyr	Ile	Tyr	Leu	Asp	Phe
305				310						315					320
Phe	Asn	Leu	Asn	Gln	Glu	Trp	Arg	Val	Tyr	Thr	Tyr	Lys	Tyr	Phe	Lys
			325						330					335	
Lys	Glu	Glu	Glu	Lys	Leu	Phe	Leu	Ala	Pro	Ile	Ser	Asp	Ser	Asp	Glu
			340					345					350		
Leu	Tyr	Asn	Thr	Ile	Gln	Ile	Lys	Glu	Tyr	Asp	Glu	Gln	Pro	Thr	Tyr
			355				360					365			
Ser	Cys	Gln	Leu	Leu	Phe	Lys	Lys	Asp	Glu	Glu	Ser	Thr	Asp	Glu	Ile
			370			375					380				
Gly	Leu	Ile	Gly	Ile	His	Arg	Phe	Tyr	Glu	Ser	Gly	Ile	Val	Phe	Glu
385				390						395					400
Glu	Tyr	Lys	Asp	Tyr	Phe	Cys	Ile	Ser	Lys	Trp	Tyr	Leu	Lys	Glu	Val
			405						410					415	
Lys	Arg	Lys	Pro	Tyr	Asn	Leu	Lys	Leu	Gly	Cys	Asn	Trp	Gln	Phe	Ile
			420					425					430		
Pro	Lys	Asp	Glu	Gly	Trp	Thr	Glu								
			435				440								

<210> 9

<211> 1371

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTC1 Hc

<400> 9

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gaattcacga tgaccatccc attcaacatc ttctcctaca ccaacaactc cctgttgaag 60
gacatcatca acgagtactt caacaacatc aacgactcca agatcctgtc cctgcagaac 120
cgtaagaaca ccttggtcga cacctccggt tacaacgccg aggtctccga ggaggggtgac 180
gtccagctga acccaatctt cccattcgac ttcaagctgg gttcctccgg tgaggacaga 240
ggtaagggtca tcgtcaccca gaacgagAAC atcgtctaca actccatgta cgagtccttc 300
tccatctcct tctggatcag aatcaacaag tgggtctcca acttgccagg ttacaccatc 360
atcgactccg tcaagaacaa ctccggttgg tccatcggtA tcatctccaa cttcctggtc 420
ttcaccctga agcagaacga ggactccgag cagtccatca acttctccta cgacatctcc 480
aacaacgctc ctggttacaa caagtggttc ttcgtcaccg tcaccaacaa catgatgggt 540
aagatgaaga tctacatcaa cggtAagctg atcgacacca tcaaggTcaa ggagttgacc 600
ggatatcaact tctccaagac catcaccttc gagatcaaca agatcccaga caccggctctg 660
atcacctccg actccgacaa catcaacatg tggatccgtg acttctacat cttcgccaag 720
gagttggacg gtaaggacat caacatcctg ttcaactcct tgcagtacac caacgtcgtc 780
aaggactact ggggtaacga cctgagatac aacaaggagt actacatggT caacatcgac 840
tacttgaaca gatacatgta cgccaactcc agacagatcg tcttcaacac cagacgtaac 900
aacaacgact tcaacgaggg ttacaagatc atcatcaagc gtatcagagg taacaccaac 960
gacaccagag tcagaggtgg tgacatcctg tacttcgaca tgactatcaa caacaaggcc 1020
tacaacctgt tcatgaagaa cgagaccatg tacgccgaca accactccac cgaggacatc 1080
tacgccatcg gtctgcgtga gcagaccaag gacatcaacg acaacatcat cttccagatc 1140
cagccaatga acaacactta ctactacgtt tcccagatct tcaagtccaa cttcaacggt 1200
gagaacatct ccggtatctg ttccatcggt acctacagat tccgtctggg tggtgactgg 1260
tacagacaca actacttggT tccaactgtc aagcagggtA actacgcctc cttgtctggag 1320
tccacttcca cccactgggg attcgtccca gtctccgagt aataggaatt c 1371
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<210> 10

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTC1 Hc

<400> 10

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Met Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu
 1           5           10           15
Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn Asp Ser Lys Ile
          20           25           30
Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp Thr Ser Gly Tyr
          35           40           45
Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu Asn Pro Ile Phe
          50           55           60
Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp Arg Gly Lys Val
65           70           75           80
Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser Met Tyr Glu Ser
          85           90           95
Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp Val Ser Asn Leu
          100          105          110
Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn Ser Gly Trp Ser
          115          120          125
Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu Lys Gln Asn Glu
          130          135          140
Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile Ser Asn Asn Ala
145          150          155          160
Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr Asn Asn Met Met
```



```

ttcttcgtca ccatcaccaa caacatcatg ggttacatga agttgtacat caacgggtgag 600
ttgaagcagt cccagaagat cgaggacctg gacgagggtca agctggacaa gaccatcgtc 660
ttcgggtatcg acgagaacat cgacgagaac cagatgttgt ggatccgtga cttcaacatc 720
ttctccaagg agctgtccaa cgaggacatc aacatcgtct acgaggggtca gatcctgagg 780
aacgtcatca aggactactg gggtaaccca ctgaagttcg acaccgagta ctacatcatc 840
aacgacaact acatcgaccg ttacatcgcc ccagagtcca acgtcctggg cctgggtccag 900
taccctgacc gttccaagct gtacaccggg aaccctatca ccatcaagtc cgtctccgac 960
aagaaccctt actcccgtat cctgaacggg gacaacatca tcctgcacat gctgtacaac 1020
tcccgttaagt acatgatcat ccgtgacacc gacaccatct acgccaccca ggggtggtgac 1080
tggtcccaga actgtgtcta cgccctgaag ctgcagtcca acctgggtaa ctacgggtatc 1140
ggtatcttct ccatcaagaa catcgtctcc aagaacaagt actgctccca gatcttctcc 1200
tccttcctgt agaaccacct gctgctggcc gacatctaca agccttggcg tttctccttc 1260
aagaacgcct acactcctgt cgccgtcacc aactacgaga ccaagctgct gtccacctcc 1320
tccttctgga agttcatctc ccgtgaccca gggtgggtcg agtaatagga attc 1374

```

<210> 12

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTD Hc

<400> 12

```

Met Arg Leu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr Met Pro
1          5          10          15
Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile
20          25          30
Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln
35          40          45
Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val
50          55          60
Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn Asp Phe
65          70          75          80
Lys Leu Ser Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn Asn Asn
85          90          95
Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe Trp Ile
100         105         110
Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr Ile Ile
115         120         125
Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg Asn Gly
130         135         140
Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys Ser Leu
145         150         155         160
Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr Asn Lys
165         170         175
Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met Lys Leu
180         185         190
Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp Leu Asp
195         200         205
Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu Asn Ile
210         215         220
Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe Ser Lys
225         230         235         240
Glu Leu Ser Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln Ile Leu
245         250         255

```

Arg	Asn	Val	Ile	Lys	Asp	Tyr	Trp	Gly	Asn	Pro	Leu	Lys	Phe	Asp	Thr
		260						265					270		
Glu	Tyr	Tyr	Ile	Ile	Asn	Asp	Asn	Tyr	Ile	Asp	Arg	Tyr	Ile	Ala	Pro
		275						280					285		
Glu	Ser	Asn	Val	Leu	Val	Leu	Val	Gln	Tyr	Pro	Asp	Arg	Ser	Lys	Leu
		290					295					300			
Tyr	Thr	Gly	Asn	Pro	Ile	Thr	Ile	Lys	Ser	Val	Ser	Asp	Lys	Asn	Pro
		305			310					315					320
Tyr	Ser	Arg	Ile	Leu	Asn	Gly	Asp	Asn	Ile	Ile	Leu	His	Met	Leu	Tyr
			325						330					335	
Asn	Ser	Arg	Lys	Tyr	Met	Ile	Ile	Arg	Asp	Thr	Asp	Thr	Ile	Tyr	Ala
			340					345					350		
Thr	Gln	Gly	Gly	Asp	Cys	Ser	Gln	Asn	Cys	Val	Tyr	Ala	Leu	Lys	Leu
		355					360					365			
Gln	Ser	Asn	Leu	Gly	Asn	Tyr	Gly	Ile	Gly	Ile	Phe	Ser	Ile	Lys	Asn
		370				375					380				
Ile	Val	Ser	Lys	Asn	Lys	Tyr	Cys	Ser	Gln	Ile	Phe	Ser	Ser	Phe	Arg
		385			390					395					400
Glu	Asn	Thr	Met	Leu	Leu	Ala	Asp	Ile	Tyr	Lys	Pro	Trp	Arg	Phe	Ser
			405						410					415	
Phe	Lys	Asn	Ala	Tyr	Thr	Pro	Val	Ala	Val	Thr	Asn	Tyr	Glu	Thr	Lys
			420					425					430		
Leu	Leu	Ser	Thr	Ser	Ser	Phe	Trp	Lys	Phe	Ile	Ser	Arg	Asp	Pro	Gly
		435					440					445			
Trp	Val	Glu													
		450													

<210> 13

<211> 1400

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTE Hc

<400> 13

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gaattcacca tgggagagag tcagcaagaa ctaaattcta tggtaactga taccctaaat 60
aatagtattc cttttaagct ttcttcttat acagatgata aaattttaat ttcttacttc 120
aacaagttct tcaagagaat taagtcttct tccgttttaa acatgagata caagaatgat 180
aaatacgtcg acacttccgg ttacgactcc aatatcaaca ttaacggtga cgtgtacaag 240
tacccaacta acaaaaacca attcggtatc tacaacgaca agcttactga gctgaacatc 300
tctcaaaaacg actacattat ctacgacaac aagtacaaga acttctctat ttctttctgg 360
gtcaggattc ctaactacga caacaagatc gtcaacgtta acaacgagta cactatcatc 420
aactgtatga gagacaacaa ctccggttgg aagggtctctc ttaaccacaa cgagatcatt 480
tggaccttgc aagacaacgc aggtattaac caaaagttag cattcaacta cggtaacgca 540
aacggtatct ctgactacat caacaagtgg attttcgtca ctatcactaa cgacagatta 600
ggtgactcta agctttacat taacggtaac ttaatcgacc aaaagtccat tttaaactta 660
ggtaacattc acgtttctga caacatctta ttcaagatcg ttaactgcag ttacaccaga 720
tacattggca ttagatactt caacattttc gacaaggagt tagacgagac cgagattcaa 780
actttataca gcaacgaacc taacaccaat attttgaagg acttctgggg taactatttg 840
ctttacgaca aggaatacta cttattaaac gtgttaaagc caaacaactt cattgatagg 900
agaaaggatt ctactttaag cattaacaac atcagaagca ctattctttt agctaacaga 960
ttatactctg gtatcaaggt taagatccaa agagttaaca actcttctac taacgataac 1020
cttgtagtaa agaacgatca ggtctatatt aacttcgctg ctagcaagac tcacttattc 1080
ccattatatg ctgataccgc taccaccaac aaggagaaga ccatcaagat ctctctctct 1140
ggcaacagat ttaaccaagt cgtcggttat aactccgctg gtaacaactg taccatgaac 1200

```

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tttaaaaata ataatggaaa taatattggg ttgtaggtt tcaaggcaga tactgtagtt 1260
gctagtactt ggtattatac ccacatgaga gatcacacca acagcaatgg atgttttttg 1320
aactttattt ctgaagaaca tggatggcaa gaaaaataat agggatccgc ggccgcacgc 1380
gtccccgggac tagtgaattc                                     1400

```

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<210> 14
<211> 449
<212> PRT
<213> Artificial Sequence

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<220>
<223> Encoded polypeptide of a synthetic construct based
      on BoNTE Hc

```

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<400> 14
Met Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr Asp Thr Leu
 1          5          10          15
Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp Asp Lys Ile
 20          25          30
Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser Ser Ser
 35          40          45
Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr Ser Gly
 50          55          60
Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr Pro Thr
 65          70          75          80
Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Thr Glu Leu Asn
 85          90          95
Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys Asn Phe
100          105          110
Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys Ile Val
115          120          125
Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp Asn Asn
130          135          140
Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp Thr Leu
145          150          155          160
Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr Gly Asn
165          170          175
Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val Thr Ile
180          185          190
Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly Asn Leu
195          200          205
Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val Ser Asp
210          215          220
Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr Ile Gly
225          230          235          240
Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr Glu Ile
245          250          255
Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys Asp Phe
260          265          270
Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu Asn Val
275          280          285
Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr Leu Ser
290          295          300
Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu Tyr Ser
305          310          315          320
Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr Asn Asp
325          330          335

```

Asn	Leu	Val	Arg	Lys	Asn	Asp	Gln	Val	Tyr	Ile	Asn	Phe	Val	Ala	Ser
			340					345					350		
Lys	Thr	His	Leu	Phe	Pro	Leu	Tyr	Ala	Asp	Thr	Ala	Thr	Thr	Asn	Lys
		355					360					365			
Glu	Lys	Thr	Ile	Lys	Ile	Ser	Ser	Ser	Gly	Asn	Arg	Phe	Asn	Gln	Val
	370				375					380					
Val	Val	Met	Asn	Ser	Val	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe	Lys	Asn
385					390					395					400
Asn	Asn	Gly	Asn	Asn	Ile	Gly	Leu	Leu	Gly	Phe	Lys	Ala	Asp	Thr	Val
			405						410					415	
Val	Ala	Ser	Thr	Trp	Tyr	Tyr	Thr	His	Met	Arg	Asp	His	Thr	Asn	Ser
			420					425					430		
Asn	Gly	Cys	Phe	Trp	Asn	Phe	Ile	Ser	Glu	Glu	His	Gly	Trp	Gln	Glu
		435					440					445			

Lys

<210> 15
 <211> 1317
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTF Hc

<400> 15

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aagaagatca aggacaactc catcttggac atgagatacg aaaacaataa gttcatcgac 120
atctccggtt acggttccaa catctccatc aacggtgacg tctacatcta ctccaccaat 180
agaaaccagt tcggaatcta ctctccaag ccttccgagg tcaacatcgc tcagaacaac 240
gacatcatct acaacggaag ataccagaac ttctccatct ccttctgggt ccgtatccca 300
aagtacttca acaagggtcaa cctgaataac gagtacacca tcatcgactg catccgtaac 360
aataactccg gatggaagat ctccctgaac tacaacaaga tcatctggac cctgcaggac 420
accgcccgtg acaatcagaa gttggtcttc aactacaccc agatgatctc catctccgac 480
tacatcaaca agtggatctt cgtcaccatc accaataacc gtttgggaaa ctccagaatc 540
tacatcaacg gtaacttgat cgacgagaag tccatctcca acttgggtga catccacgtc 600
tccgacaaca ttttgttcaa gatcgtcggt tgtaacgaca cccggttacgt cgggatccgt 660
tacttcaaag tcttcgacac tgagttgggt aagaccgaga tcgagacctt gtactccgac 720
gagcctgacc catccatcct gaaggacttc tggggtaact acctgctgta caacaaacgt 780
tactacttgc tgaacttggt gcgtaccgac aagtccatca cccagaactc caacttcttg 840
aacatcaacc agcagagagg tgtctaccag aagccaaaca tcttctccaa caccagattg 900
tacaccggag tcgaggtcat tatcagaaag aacggatcta ctgatatttc caacaccgat 960
aacttcgtca gaaagaacga tctggcttac atcaacgttg tcgacagaga tgtcgaatac 1020
cgtctgtacg ccgatatctc tatcgccaaa cctgaaaaga tcatcaagct gatccgtacc 1080
tctaactcta acaactctct gggacaaatc atcgatcagg actccatcgg taataactgt 1140
accatgaact tccagaacaa caacggtgga aacatcggtt tggtgggttt ccactccaac 1200
aacttggtcg ctctctcttg gtactacaac aacatccgta agaacacctc ctccaacggt 1260
tgcttctggt ccttcatctc caaggagcac ggttggcagg agaactaata ggaattc 1317

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<210> 16
 <211> 432
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Encoded polypeptide of a synthetic construct based

on BoNTF Hc

<400> 16

Met	Ser	Tyr	Thr	Asn	Asp	Lys	Ile	Leu	Ile	Leu	Tyr	Phe	Asn	Lys	Leu
1				5				10						15	
Tyr	Lys	Lys	Ile	Lys	Asp	Asn	Ser	Ile	Leu	Asp	Met	Arg	Tyr	Glu	Asn
			20					25					30		
Asn	Lys	Phe	Ile	Asp	Ile	Ser	Gly	Tyr	Gly	Ser	Asn	Ile	Ser	Ile	Asn
		35					40					45			
Gly	Asp	Val	Tyr	Ile	Tyr	Ser	Thr	Asn	Arg	Asn	Gln	Phe	Gly	Ile	Tyr
	50					55					60				
Ser	Ser	Lys	Pro	Ser	Glu	Val	Asn	Ile	Ala	Gln	Asn	Asn	Asp	Ile	Ile
65					70					75					80
Tyr	Asn	Gly	Arg	Tyr	Gln	Asn	Phe	Ser	Ile	Ser	Phe	Trp	Val	Arg	Ile
				85					90					95	
Pro	Lys	Tyr	Phe	Asn	Lys	Val	Asn	Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile
			100					105					110		
Asp	Cys	Ile	Arg	Asn	Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser	Leu	Asn	Tyr
		115					120					125			
Asn	Lys	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Ala	Gly	Asn	Asn	Gln	Lys
	130					135					140				
Leu	Val	Phe	Asn	Tyr	Thr	Gln	Met	Ile	Ser	Ile	Ser	Asp	Tyr	Ile	Asn
145					150					155					160
Lys	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Gly	Asn	Ser	Arg
			165						170					175	
Ile	Tyr	Ile	Asn	Gly	Asn	Leu	Ile	Asp	Glu	Lys	Ser	Ile	Ser	Asn	Leu
		180						185					190		
Gly	Asp	Ile	His	Val	Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile	Val	Gly	Cys
	195						200					205			
Asn	Asp	Thr	Arg	Tyr	Val	Gly	Ile	Arg	Tyr	Phe	Lys	Val	Phe	Asp	Thr
	210					215					220				
Glu	Leu	Gly	Lys	Thr	Glu	Ile	Glu	Thr	Leu	Tyr	Ser	Asp	Glu	Pro	Asp
225					230					235					240
Pro	Ser	Ile	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr	Asn	Lys
			245						250					255	
Arg	Tyr	Tyr	Leu	Leu	Asn	Leu	Leu	Arg	Thr	Asp	Lys	Ser	Ile	Thr	Gln
			260						265				270		
Asn	Ser	Asn	Phe	Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val	Tyr	Gln	Lys
		275					280					285			
Pro	Asn	Ile	Phe	Ser	Asn	Thr	Arg	Leu	Tyr	Thr	Gly	Val	Glu	Val	Ile
	290					295					300				
Ile	Arg	Lys	Asn	Gly	Ser	Thr	Asp	Ile	Ser	Asn	Thr	Asp	Asn	Phe	Val
305				310						315					320
Arg	Lys	Asn	Asp	Leu	Ala	Tyr	Ile	Asn	Val	Val	Asp	Arg	Asp	Val	Glu
			325						330					335	
Tyr	Arg	Leu	Tyr	Ala	Asp	Ile	Ser	Ile	Ala	Lys	Pro	Glu	Lys	Ile	Ile
		340						345					350		
Lys	Leu	Ile	Arg	Thr	Ser	Asn	Ser	Asn	Asn	Ser	Leu	Gly	Gln	Ile	Ile
		355					360					365			
Val	Met	Asp	Ser	Ile	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe	Gln	Asn	Asn
	370					375					380				
Asn	Gly	Gly	Asn	Ile	Gly	Leu	Leu	Gly	Phe	His	Ser	Asn	Asn	Leu	Val
385					390					395					400
Ala	Ser	Ser	Trp	Tyr	Tyr	Asn	Asn	Ile	Arg	Lys	Asn	Thr	Ser	Ser	Asn
			405						410					415	
Gly	Cys	Phe	Trp	Ser	Phe	Ile	Ser	Lys	Glu	His	Gly	Trp	Gln	Glu	Asn
			420					425					430		

<210> 17
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTG Hc

<400> 17
gaattcacga tgaaggacac catcctgata cagggtcttca acaactacat ctccaacatc 60
tcttccaacg ccatcctgtc cctgtcctac cgtgggtggc gtctgatcga ctctccgggt 120
tacggagcca ccatgaacgt cggttccgac gtcattcttca acgacatcgg taacggtcag 180
ttcaagctga acaactccga gaactccaac atcacgcgcc accagtccaa gttcgtcgtc 240
tacgactcca tgttcgacaa cttctccatc aatttctggg tccgtacccc aaagtacaac 300
aacaacgaca tccagacctc cctgcagaac gactacacca tcatctcctg tatcaagaac 360
gactccgggtt ggaagggtctc catcaaggga aaccgtatca tctggaccct gatcgacgtc 420
aacgccaagt ccaagtccat cttcttcgag tactccatca aggacaacat ctccgactac 480
atcaacaagt ggttctccat caccatcacc aacgaccgtc tgggtaacgc caacatctac 540
atcaacgggtt ccctgaagaa gtccgagaag atcctgaacc tggaccgtat caactcctcc 600
aacgacatcg acttcaagct gatcaactgt accgacacca ccaagttcgt ctggatcaag 660
gacttcaaca tcttcgggtc tgagctgaac gccaccgagg tctcctccct gtactggatc 720
cagtcttcca ccaacaccct gaaggacttc tggggaaacc cactgcgtta cgacaccag 780
tactacctgt tcaaccaggg tatgcagaac atctacatca agtacttctc caaggcctcc 840
atgggtgaga ccgcccctcg taccaacttc aacaacgccc ccatcaacta ccagaacctg 900
tacctgggtc tgcgtttcat catcaagaag gcctccaact cccgtaacat caacaacgac 960
aacatcgtcc gtgaggggtga ctacatctac ctgaacatcg acaacatctc cgacgagtcc 1020
taccgtgtct acgtcctggt caactccaag gagatccaga cccagctggt cctggcccca 1080
atcaacgacg accctacctt ctacgacgtc ctgcagatca agaagtacta cgagaagacc 1140
acctacaact gtcagatcct gtgcgagaag gacaccaaga ccttcggact gttcgggtatc 1200
ggtaagttcg tcaaggacta cggttacgtc tgggacacct acgacaacta cttctgtatc 1260
tcccagtggt acctgcgtcg tatctccgag aacatcaaca agctgcgtct gggatgtaac 1320
tggcagttca tcccagtcga cgagggttgg accgagtaat aggaattc 1368

<210> 18
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTG Hc

<400> 18
Met Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile Ser Asn
1 5 10 15
Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly Arg Leu
20 25 30
Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser Asp Val
35 40 45
Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn Ser Glu
50 55 60
Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr Asp Ser
65 70 75 80
Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro Lys Tyr
85 90 95

Asn	Asn	Asn	Asp	Ile	Gln	Thr	Tyr	Leu	Gln	Asn	Glu	Tyr	Thr	Ile	Ile
			100					105					110		
Ser	Cys	Ile	Lys	Asn	Asp	Ser	Gly	Trp	Lys	Val	Ser	Ile	Lys	Gly	Asn
		115					120					125			
Arg	Ile	Ile	Trp	Thr	Leu	Ile	Asp	Val	Asn	Ala	Lys	Ser	Lys	Ser	Ile
	130					135					140				
Phe	Phe	Glu	Tyr	Ser	Ile	Lys	Asp	Asn	Ile	Ser	Asp	Tyr	Ile	Asn	Lys
145					150					155					160
Trp	Phe	Ser	Ile	Thr	Ile	Thr	Asn	Asp	Arg	Leu	Gly	Asn	Ala	Asn	Ile
			165					170						175	
Tyr	Ile	Asn	Gly	Ser	Leu	Lys	Lys	Ser	Glu	Lys	Ile	Leu	Asn	Leu	Asp
		180						185					190		
Arg	Ile	Asn	Ser	Ser	Asn	Asp	Ile	Asp	Phe	Lys	Leu	Ile	Asn	Cys	Thr
		195					200					205			
Asp	Thr	Thr	Lys	Phe	Val	Trp	Ile	Lys	Asp	Phe	Asn	Ile	Phe	Gly	Arg
	210					215					220				
Glu	Leu	Asn	Ala	Thr	Glu	Val	Ser	Ser	Leu	Tyr	Trp	Ile	Gln	Ser	Ser
225					230					235					240
Thr	Asn	Thr	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Pro	Leu	Arg	Tyr	Asp	Thr
			245						250					255	
Gln	Tyr	Tyr	Leu	Phe	Asn	Gln	Gly	Met	Gln	Asn	Ile	Tyr	Ile	Lys	Tyr
			260					265					270		
Phe	Ser	Lys	Ala	Ser	Met	Gly	Glu	Thr	Ala	Pro	Arg	Thr	Asn	Phe	Asn
		275					280					285			
Asn	Ala	Ala	Ile	Asn	Tyr	Gln	Asn	Leu	Tyr	Leu	Gly	Leu	Arg	Phe	Ile
	290					295					300				
Ile	Lys	Lys	Ala	Ser	Asn	Ser	Arg	Asn	Ile	Asn	Asn	Asp	Asn	Ile	Val
305					310					315					320
Arg	Glu	Gly	Asp	Tyr	Ile	Tyr	Leu	Asn	Ile	Asp	Asn	Ile	Ser	Asp	Glu
			325						330					335	
Ser	Tyr	Arg	Val	Tyr	Val	Leu	Val	Asn	Ser	Lys	Glu	Ile	Gln	Thr	Gln
			340					345					350		
Leu	Phe	Leu	Ala	Pro	Ile	Asn	Asp	Asp	Pro	Thr	Phe	Tyr	Asp	Val	Leu
		355					360					365			
Gln	Ile	Lys	Lys	Tyr	Tyr	Glu	Lys	Thr	Thr	Tyr	Asn	Cys	Gln	Ile	Leu
	370					375					380				
Cys	Glu	Lys	Asp	Thr	Lys	Thr	Phe	Gly	Leu	Phe	Gly	Ile	Gly	Lys	Phe
385					390					395					400
Val	Lys	Asp	Tyr	Gly	Tyr	Val	Trp	Asp	Thr	Tyr	Asp	Asn	Tyr	Phe	Cys
			405						410					415	
Ile	Ser	Gln	Trp	Tyr	Leu	Arg	Arg	Ile	Ser	Glu	Asn	Ile	Asn	Lys	Leu
		420						425				430			
Arg	Leu	Gly	Cys	Asn	Trp	Gln	Phe	Ile	Pro	Val	Asp	Glu	Gly	Trp	Thr
		435					440					445			

Glu

<210> 19

<211> 1242

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTA Hn

<400> 19

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atggctctga acgacctgtg catcaaagtt aacaactggg acctgttctt ctccccgtct 60
gaagacaact tcactaacga cctgaacaaa ggccaagaaa tcacctccga cactaacatc 120
gaagctgctg aagaaaacat ctctctggac ctgatccagc agtactacct gactttcaac 180
ttcgacaacg aaccggaaaa catctccatc gaaaacctgt ctcccgacat catcggtcag 240
ctggaactga tgccgaacat cgaacgcttc ccgaacggca agaaatacga actggacaaa 300
tacaccatgt tccactacct gcgtgctcag gaattcgaac acggtaaatac tcgtatcgct 360
ctgactaact ccgttaacga agctctgctg aaccctgtct gcgtttacac cttcttctct 420
tccgactacg ttaagaaagt taacaaagct actgaagctg ctatgttcct ggggtgggtt 480
gaacagctgg tttacgactt caccgaacga acttctgaag tttccaccac tgacaaaatc 540
gctgacatca ctatcatcat cccgtacatc ggcccggctc tgaacatcgg taacatgctg 600
tacaaagacg acttcgttgg tgctctgac ttctctggcg ctgttatcct gctggaattc 660
atccccgaaa tcgctatccc gggtctgggt accttcgctc tggtttccta catcgctaac 720
aaagttctga ctgttcagac catcgacaac gctctgtcta aacgtaacga aaaatgggac 780
gaagttttaca aatacatcgt tactaactgg ctggctaaag ttaacactca gatcgacctg 840
atccgtaaga agatgaaaga agctctggaa aaccaggctg aagctactaa agctatcatc 900
aactaccagt acaaccagta caccgaagaa gaaaagaaca acatcaactt caacatcgat 960
gacctgtcct ctaaactgaa cgaatccatc aacaaagcta tgatcaacat caacaaattc 1020
ctgaaccagt gctctgtttc ctacctgatg aactctatga tcccgtacgg cgttaaacgc 1080
ctggaagact tcgacgcttc cctgaaagac gctctgctga aatacatccg tgacaactac 1140
gggtactctga tcggccaggt tgaccgtctg aaagacaagg ttaacaacac cctgtctact 1200
gacatcccgt tccagctgtc caaatacgtt gacaaccagt aa 1242

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<210> 20

<211> 413

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTA Hn

<400> 20

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Met Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe
 1              5              10              15
Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu
              20              25              30
Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser
              35              40              45
Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu
              50              55              60
Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln
65              70              75              80
Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr
              85              90              95
Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe
              100             105             110
Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala
              115             120             125
Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val
              130             135             140
Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val
145             150             155             160
Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr
              165             170             175
Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro
              180             185             190
Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala

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	195		200		205										
Leu	Ile	Phe	Ser	Gly	Ala	Val	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Ile
	210						215				220				
Ala	Ile	Pro	Val	Leu	Gly	Thr	Phe	Ala	Leu	Val	Ser	Tyr	Ile	Ala	Asn
225					230					235					240
Lys	Val	Leu	Thr	Val	Gln	Thr	Ile	Asp	Asn	Ala	Leu	Ser	Lys	Arg	Asn
				245					250					255	
Glu	Lys	Trp	Asp	Glu	Val	Tyr	Lys	Tyr	Ile	Val	Thr	Asn	Trp	Leu	Ala
			260					265					270		
Lys	Val	Asn	Thr	Gln	Ile	Asp	Leu	Ile	Arg	Lys	Lys	Met	Lys	Glu	Ala
		275					280					285			
Leu	Glu	Asn	Gln	Ala	Glu	Ala	Thr	Lys	Ala	Ile	Ile	Asn	Tyr	Gln	Tyr
	290					295					300				
Asn	Gln	Tyr	Thr	Glu	Glu	Glu	Lys	Asn	Asn	Ile	Asn	Phe	Asn	Ile	Asp
305					310					315					320
Asp	Leu	Ser	Ser	Lys	Leu	Asn	Glu	Ser	Ile	Asn	Lys	Ala	Met	Ile	Asn
				325					330					335	
Ile	Asn	Lys	Phe	Leu	Asn	Gln	Cys	Ser	Val	Ser	Tyr	Leu	Met	Asn	Ser
			340					345					350		
Met	Ile	Pro	Tyr	Gly	Val	Lys	Arg	Leu	Glu	Asp	Phe	Asp	Ala	Ser	Leu
	355					360					365				
Lys	Asp	Ala	Leu	Leu	Lys	Tyr	Ile	Arg	Asp	Asn	Tyr	Gly	Thr	Leu	Ile
	370					375					380				
Gly	Gln	Val	Asp	Arg	Leu	Lys	Asp	Lys	Val	Asn	Asn	Thr	Leu	Ser	Thr
385					390					395					400
Asp	Ile	Pro	Phe	Gln	Leu	Ser	Lys	Tyr	Val	Asp	Asn	Gln			
			405						410						

<210> 21
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTB Hn

<400> 21
 atggctccag gaatctgtat cgacgtcgac aacgaggact tggtcttcat cgctgacaag 60
 aactccttct cgcacgactt gtccaagaac gagagaatcg agtacaacac ccagtccaac 120
 tacatcgaga acgacttccc aatcaacgag ttgatcttgg acaccgactt gatctccaag 180
 atcgagttgc catccgagaa caccgagtc ttgactgact tcaacgtcga cgtcccagtc 240
 tacgagaagc aaccagctat caagaagatt ttcaccgacg agaacaccat cttccaatac 300
 ctgtactctc agaccttccc tttggacatc agagacatct cttgacctc ttccttcgac 360
 gacgccctgc tggtctccaa caaggtctac tccttcttct ccatggacta catcaagact 420
 gctaacaagg tcgtcgaggc cggtttggtc gctggttggg tcaagcagat cgtcaacgat 480
 ttctgcatcg aggtaacaa gtccaacacc atggacaaga ttgccgacat ctctttgatt 540
 gtcccatata tcggtttggc cttgaacgtc ggtaacgaga ccgccaaggg taacttcgag 600
 aacgctttcg agatcgctgg tgcctccatc ttggtggagt tcatccaga gttgttgatc 660
 ccagtcgtcg gtgccttctt gttggagtcc tacatcgaca acaagaacaa gatcatcaag 720
 accatcgaca acgctttgac caagagaaac gagaagtggc ccgacatgta cggtttgatc 780
 gtcgcccaat ggttgctcac cgtcaacacc caattctaca ccatcaagga gggatgtac 840
 aaggccttga actaccaggc ccaagctttg gaggagatca tcaagtacag atacaacatc 900
 tactccgaga aggagaagtc caacattaac atcgacttca acgacatcaa ctccaagctg 960
 aacgagggtg ttaaccaggc catcgacaac atcaacaact tcatcaacgg ttgttccgtc 1020
 tcctacttga tgaagaagat gattccattg gccgtcgaga agttgttgga cttcgacaac 1080
 accctgaaga agaacttggt gaactacatc gacgagaaca agttgtactt gatcggttcc 1140

gctgagtacg agaagtccaa ggtcaacaag tacttgaaga ccatcatgcc attcgacttg 1200
 tccatctaca ccaacgacac catcttgatc gagatgttct aa 1242

<210> 22
 <211> 413
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Encoded polypeptide of a synthetic construct based
 on BoNTB Hn

<400> 22
 Met Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe
 1 5 10 15
 Ile Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg
 20 25 30
 Ile Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile
 35 40 45
 Asn Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro
 50 55 60
 Ser Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val
 65 70 75 80
 Tyr Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr
 85 90 95
 Ile Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp
 100 105 110
 Ile Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys
 115 120 125
 Val Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val
 130 135 140
 Val Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp
 145 150 155 160
 Phe Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp
 165 170 175
 Ile Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn
 180 185 190
 Glu Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala
 195 200 205
 Ser Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly
 210 215 220
 Ala Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys
 225 230 235 240
 Thr Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met
 245 250 255
 Tyr Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe
 260 265 270
 Tyr Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln
 275 280 285
 Ala Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys
 290 295 300
 Glu Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu
 305 310 315 320
 Asn Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn
 325 330 335
 Gly Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val
 340 345 350

Pro Asp Asn Val Ser Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser
 50 55 60
 Glu His Gly Gln Leu Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser
 65 70 75 80
 Glu Ile Leu Pro Gly Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln
 85 90 95
 Asn Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu
 100 105 110
 Ser Asp Asn Val Glu Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala
 115 120 125
 Leu Asp Asn Ser Ala Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn
 130 135 140
 Lys Val Asn Ala Gly Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn
 145 150 155 160
 Asp Val Val Glu Asp Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu
 165 170 175
 Asp Lys Ile Ser Asp Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala
 180 185 190
 Leu Asn Ile Ser Asn Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe
 195 200 205
 Ala Val Thr Gly Val Thr Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr
 210 215 220
 Ile Pro Ala Leu Gly Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg
 225 230 235 240
 Asn Glu Ile Ile Lys Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys
 245 250 255
 Arg Trp Lys Asp Ser Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg
 260 265 270
 Ile Ile Thr Gln Phe Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu
 275 280 285
 Asn Tyr Gln Ala Gly Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys
 290 295 300
 Lys Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn
 305 310 315 320
 Leu Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile
 325 330 335
 Asn Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met
 340 345 350
 Leu Pro Lys Val Ile Asp Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys
 355 360 365
 Ala Lys Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly
 370 375 380
 Glu Val Asp Lys Leu Lys Ala Lys Val Asn Asn Ser Phe Gln Asn
 385 390 395

<210> 25

<211> 1161

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTD Hn

<400> 25

atggccaact cccgtgacga ctccacctgc atcaaggtca agaacaacag actgccatac 60
 gttgccgaca aggactccat ctcccaggag atcttcgaga acaagatcat caccgacgag 120

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accaacgttc aaaactactc cgacaagttc tctttggacg agtccatcct ggacgggtcag 180
gtcccaatca acccagagat cgtcgaccca ctggttgccaa acgtcaacat ggagccattg 240
aacttgccag gtgaggagat cgtcttctac gacgacatca ccaagtacgt cgactacttg 300
aactcctact actacttgga gtctcaaaag ttgtctaaca acgtcgagaa catcaccttg 360
accacctccg tcgaggaggc cttggggttac tctaacaaga tctacacctt cctgccatcc 420
ttggctgaga aggttaacaa ggggtgttcaa gctgggttgt tcctgaactg ggccaacgag 480
gtcgtcgagg acttcaccac caacatcatg aagaaggaca ccctggacaa gatctccgac 540
gtctccgtca tcatcccata catcgggtcca gccttgaaca tcggtaactc cgccctgaga 600
ggtaacttca accaggcctt cgccaccgcc ggtgtgcctt tcctgctgga gggtttccca 660
gagttcacca tccagccctt ggggtgtctt accttctact cctccatcca ggagagagag 720
aagatcatca agaccatcga gaactgcttg gagcagagag tcaagagatg gaaggactcc 780
taccagtgga tggtttccaa ctggctgtcc agaataacca cccaattcaa ccacatcaac 840
taccagatgt acgactccct gtcctaccag gccgacgcca tcaaggccaa gatcgacctg 900
gagtacaaga agtactccgg ttccgacaag gagaacatca agtcccaggt cgagaacctg 960
aagaactcct tggacgtcaa gatctccgag gccatgaaca acatcaacaa gttcatccgt 1020
gagtgttccg tcacctacct gttcaagaac atgctgccaa aggtcatcga cgagctgaac 1080
aagttcgacc tgagaaccaa gaccgagctg atcaacctga tcgactccca caacatcatc 1140
ctggttggtg aggttgacta a                                     1161

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<210> 26

<211> 386

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTD Hn

<400> 26

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Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn
 1               5               10               15
Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe
      20               25               30
Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp
      35               40               45
Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn
      50               55               60
Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu
      65               70               75               80
Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr
      85               90               95
Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser
      100              105              110
Asn Asn Val Glu Asn Ile Thr Leu Thr Thr Ser Val Glu Glu Ala Leu
      115              120              125
Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys
      130              135              140
Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu
      145              150              155              160
Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp
      165              170              175
Lys Ile Ser Asp Val Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu
      180              185              190
Asn Ile Gly Asn Ser Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala
      195              200              205
Thr Ala Gly Val Ala Phe Leu Leu Glu Gly Phe Pro Glu Phe Thr Ile
      210              215              220

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Pro Ala Leu Gly Val Phe Thr Phe Tyr Ser Ser Ile Gln Glu Arg Glu
 225 230 235 240
 Lys Ile Ile Lys Thr Ile Glu Asn Cys Leu Glu Gln Arg Val Lys Arg
 245 250 255
 Trp Lys Asp Ser Tyr Gln Trp Met Val Ser Asn Trp Leu Ser Arg Ile
 260 265 270
 Thr Thr Gln Phe Asn His Ile Asn Tyr Gln Met Tyr Asp Ser Leu Ser
 275 280 285
 Tyr Gln Ala Asp Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys
 290 295 300
 Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu
 305 310 315 320
 Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn
 325 330 335
 Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu
 340 345 350
 Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr
 355 360 365
 Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu
 370 375 380
 Val Asp
 385

<210> 27
 <211> 1149
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTE Hn

<400> 27
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 tacaacgatg acaacatcaa cactcctaag gagattgacg acaccgtcac ttctaacaac 120
 aactacgaaa acgacctgga ccagggtcatc ctaaacttca actccgagtc cgcccctggt 180
 ctgtccgacg agaagctgaa cctgaccatc cagaacgacg cttacatccc aaagtacgac 240
 tccaacggta catccgatat cgagcagcat gacgttaacg agcttaacgt cttctttctac 300
 ttagacgctc agaaggtgcc cgaggggtgag aacaacgtca atctcacctc ttcaattgac 360
 acagccttgt tggagcagcc taagatctac accttcttct cctccgagtt catcaacaac 420
 gtcaacaagc ctgtgcaggc cgcattgttc gtaagctgga ttcagcaggt gttagtagac 480
 ttcactactg aggctaacca gaagtccact gttgacaaga tcgctgacat ctccatcgtc 540
 gtcccataca tcggtctggc tctgaacatc ggcaacgagg cacagaaggg caacttcaag 600
 gatgcccttg agttgttggg tgccggtatt ttgttggagt tcgaaccgga gctgctgac 660
 cctaccatcc tggctcttcac gatcaagtc ttcttggtt cctccgacaa caagaacaag 720
 gtcattaagg ccatcaacaa cgccctgaag gagcgtgacg agaagtggaa ggaagtctat 780
 tccttcatcg tctcgaactg gatgaccaag atcaacaccc agttcaacaa gcgaaaggag 840
 cagatgtacc aggctctgca gaaccaggtc aacgccatca agaccatcat cgagtccaag 900
 tacaactcct acaccctgga ggagaagaac gagcttacca acaagtacga tatcaagcag 960
 atcgagaacg agctgaacca gaaggtctcc atcgccatga acaacatcga caggttcctg 1020
 accgagtcct ccatctccta cctgatgaag ctcatcaacg aggtcaagat caacaagctg 1080
 cgagagtacg acgagaatgt caagacgtac ctgctgaact acatcatcca gcacggatcc 1140
 atcctgtaa 1149

<210> 28
 <211> 382
 <212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTE Hn

<400> 28

Met	Ser	Ile	Cys	Ile	Glu	Ile	Asn	Asn	Gly	Glu	Leu	Phe	Phe	Val	Ala
1				5					10					15	
Ser	Glu	Asn	Ser	Tyr	Asn	Asp	Asp	Asn	Ile	Asn	Thr	Pro	Lys	Glu	Ile
			20					25					30		
Asp	Asp	Thr	Val	Thr	Ser	Asn	Asn	Asn	Tyr	Glu	Asn	Asp	Leu	Asp	Gln
		35					40					45			
Val	Ile	Leu	Asn	Phe	Asn	Ser	Glu	Ser	Ala	Pro	Gly	Leu	Ser	Asp	Glu
	50					55					60				
Lys	Leu	Asn	Leu	Thr	Ile	Gln	Asn	Asp	Ala	Tyr	Ile	Pro	Lys	Tyr	Asp
65					70					75					80
Ser	Asn	Gly	Thr	Ser	Asp	Ile	Glu	Gln	His	Asp	Val	Asn	Glu	Leu	Asn
				85					90					95	
Val	Phe	Phe	Tyr	Leu	Asp	Ala	Gln	Lys	Val	Pro	Glu	Gly	Glu	Asn	Asn
			100					105					110		
Val	Asn	Leu	Thr	Ser	Ser	Ile	Asp	Thr	Ala	Leu	Leu	Glu	Gln	Pro	Lys
	115						120					125			
Ile	Tyr	Thr	Phe	Phe	Ser	Ser	Glu	Phe	Ile	Asn	Asn	Val	Asn	Lys	Pro
	130					135					140				
Val	Gln	Ala	Ala	Leu	Phe	Val	Ser	Trp	Ile	Gln	Gln	Val	Leu	Val	Asp
145					150					155					160
Phe	Thr	Thr	Glu	Ala	Asn	Gln	Lys	Ser	Thr	Val	Asp	Lys	Ile	Ala	Asp
				165					170					175	
Ile	Ser	Ile	Val	Val	Pro	Tyr	Ile	Gly	Leu	Ala	Leu	Asn	Ile	Gly	Asn
			180					185					190		
Glu	Ala	Gln	Lys	Gly	Asn	Phe	Lys	Asp	Ala	Leu	Glu	Leu	Leu	Gly	Ala
	195						200					205			
Gly	Ile	Leu	Leu	Glu	Phe	Glu	Pro	Glu	Leu	Leu	Ile	Pro	Thr	Ile	Leu
	210					215					220				
Val	Phe	Thr	Ile	Lys	Ser	Phe	Leu	Gly	Ser	Ser	Asp	Asn	Lys	Asn	Lys
225					230					235					240
Val	Ile	Lys	Ala	Ile	Asn	Asn	Ala	Leu	Lys	Glu	Arg	Asp	Glu	Lys	Trp
			245						250					255	
Lys	Glu	Val	Tyr	Ser	Phe	Ile	Val	Ser	Asn	Trp	Met	Thr	Lys	Ile	Asn
		260						265					270		
Thr	Gln	Phe	Asn	Lys	Arg	Lys	Glu	Gln	Met	Tyr	Gln	Ala	Leu	Gln	Asn
	275					280						285			
Gln	Val	Asn	Ala	Ile	Lys	Thr	Ile	Ile	Glu	Ser	Lys	Tyr	Asn	Ser	Tyr
	290					295					300				
Thr	Leu	Glu	Glu	Lys	Asn	Glu	Leu	Thr	Asn	Lys	Tyr	Asp	Ile	Lys	Gln
305					310					315					320
Ile	Glu	Asn	Glu	Leu	Asn	Gln	Lys	Val	Ser	Ile	Ala	Met	Asn	Asn	Ile
			325						330					335	
Asp	Arg	Phe	Leu	Thr	Glu	Ser	Ser	Ile	Ser	Tyr	Leu	Met	Lys	Leu	Ile
		340						345					350		
Asn	Glu	Val	Lys	Ile	Asn	Lys	Leu	Arg	Glu	Tyr	Asp	Glu	Asn	Val	Lys
	355						360					365			
Thr	Tyr	Leu	Leu	Asn	Tyr	Ile	Ile	Gln	His	Gly	Ser	Ile	Leu		
	370					375					380				

<210> 29
 <211> 1227
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTF Hn

<400> 29
 atggccccac cacgtctgtg tattagagtc aacaactcag aattattctt tgctcgttcc 60
 gagtcaagct acaacgagaa cgatattaac acacctaaag agattgacga tactaccaac 120
 ctaaacaaca actaccgga caacttggat gaggttattt tggattacaa ctacagacc 180
 atccctcaaa tttccaaccg taccttaaac actcttgctc aagacaactc ctacgttcca 240
 agatacgatt ctaacggtac ctcagagatc gaggagtatg atgttggtga ctttaacgtc 300
 tttttctatt tgcattgcca gaagggtgcca gaagggtgaaa ccaacatctc attgacttct 360
 tccattgata cgccttggtt ggaagagtcc aaggatatct tcttttcttc ggagtttatt 420
 gatactatca acaagcctgt caacgcctgt ctgttcattg attggattag caagggtcatc 480
 agagatttta ccaactgaagc tactcaaaag tccactgttg ataagattgc tgacatctct 540
 ttgattgtcc cctatgtcgg tcttgctttg aacatcatta ttgaggcaga aaagggtaac 600
 tttgaggagg cttttgaatt gttgggagtt ggtattttgt tggagtttgt tccagaactt 660
 accattcctg tcatttttagt ttttacgac aagtcctaca tcgattcata cgagaacaag 720
 aataaagcaa ttaaagctat taacaactcc ttgatcgaaa gagaggctaa gtggaaggaa 780
 atctactcat ggattgtatc aaactggctt actagaatta acactcaatt taacaagaga 840
 aaggagcaaa tgtaccaggc tctgcaaaac caagtcgatg ctatcaagac tgcaattgaa 900
 tacaagtaca acaactatac ttccgatgag aagaacagac ttgaatctga atacaatatc 960
 aacaacattg aagaagagtt gaacaagaaa gtttcttttg ctatgaagaa tatcgaaaga 1020
 tttatgaccg aatcctctat ctcttacttg atgaagttga tcaatgaggc caagggttgt 1080
 aagttgaaga agtacgataa ccacgttaag agcgatctgc tgaactacat tctcgaccac 1140
 agatcaatcc tgggagagca gacaaacgag ctgagtgtatt tggttacttc cactttgaac 1200
 tcttccattc catttgagct ttcttaa 1227

<210> 30
 <211> 408
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Encoded polypeptide of a synthetic construct based
 on BoNTF Hn

<400> 30
 Met Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn Ser Glu Leu Phe
 1 5 10 15
 Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro
 20 25 30
 Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Asn Tyr Arg Asn Asn
 35 40 45
 Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Gln Thr Ile Pro Gln Ile
 50 55 60
 Ser Asn Arg Thr Leu Asn Thr Leu Val Gln Asp Asn Ser Tyr Val Pro
 65 70 75 80
 Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu Tyr Asp Val Val
 85 90 95
 Asp Phe Asn Val Phe Phe Tyr Leu His Ala Gln Lys Val Pro Glu Gly
 100 105 110
 Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu
 115 120 125

Glu	Ser	Lys	Asp	Ile	Phe	Phe	Ser	Ser	Glu	Phe	Ile	Asp	Thr	Ile	Asn
130						135					140				
Lys	Pro	Val	Asn	Ala	Ala	Leu	Phe	Ile	Asp	Trp	Ile	Ser	Lys	Val	Ile
145					150					155					160
Arg	Asp	Phe	Thr	Thr	Glu	Ala	Thr	Gln	Lys	Ser	Thr	Val	Asp	Lys	Ile
			165						170					175	
Ala	Asp	Ile	Ser	Leu	Ile	Val	Pro	Tyr	Val	Gly	Leu	Ala	Leu	Asn	Ile
			180					185					190		
Ile	Ile	Glu	Ala	Glu	Lys	Gly	Asn	Phe	Glu	Glu	Ala	Phe	Glu	Leu	Leu
	195						200					205			
Gly	Val	Gly	Ile	Leu	Leu	Glu	Phe	Val	Pro	Glu	Leu	Thr	Ile	Pro	Val
	210					215					220				
Ile	Leu	Val	Phe	Thr	Ile	Lys	Ser	Tyr	Ile	Asp	Ser	Tyr	Glu	Asn	Lys
225					230					235					240
Asn	Lys	Ala	Ile	Lys	Ala	Ile	Asn	Asn	Ser	Leu	Ile	Glu	Arg	Glu	Ala
			245						250					255	
Lys	Trp	Lys	Glu	Ile	Tyr	Ser	Trp	Ile	Val	Ser	Asn	Trp	Leu	Thr	Arg
			260					265					270		
Ile	Asn	Thr	Gln	Phe	Asn	Lys	Arg	Lys	Glu	Gln	Met	Tyr	Gln	Ala	Leu
		275				280						285			
Gln	Asn	Gln	Val	Asp	Ala	Ile	Lys	Thr	Ala	Ile	Glu	Tyr	Lys	Tyr	Asn
	290					295					300				
Asn	Tyr	Thr	Ser	Asp	Glu	Lys	Asn	Arg	Leu	Glu	Ser	Glu	Tyr	Asn	Ile
305					310					315					320
Asn	Asn	Ile	Glu	Glu	Glu	Leu	Asn	Lys	Lys	Val	Ser	Leu	Ala	Met	Lys
			325						330					335	
Asn	Ile	Glu	Arg	Phe	Met	Thr	Glu	Ser	Ser	Ile	Ser	Tyr	Leu	Met	Lys
			340					345					350		
Leu	Ile	Asn	Glu	Ala	Lys	Val	Gly	Lys	Leu	Lys	Lys	Tyr	Asp	Asn	His
		355					360					365			
Val	Lys	Ser	Asp	Leu	Leu	Asn	Tyr	Ile	Leu	Asp	His	Arg	Ser	Ile	Leu
	370					375					380				
Gly	Glu	Gln	Thr	Asn	Glu	Leu	Ser	Asp	Leu	Val	Thr	Ser	Thr	Leu	Asn
385					390					395					400
Ser	Ser	Ile	Pro	Phe	Glu	Leu	Ser								
				405											

<210> 31
 <211> 1233
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTG Hn

<400> 31
 atggccaaaa ataccggttaa atctgaacag tgtattattg ttaataatga ggatttattt 60
 ttcataagcta ataaagatag tttttcaaaa gatttagcta aagcagaaac tatagcatat 120
 aatacacaaa ataatactat agaaaataat ttttctatag atcagttgat tttagataat 180
 gatttaagca gtggcataga cttaccaa atgaaaacacag aaccatttac aaattttgac 240
 gacataagata tcctgtgtta tattaacaa tctgctttta aaaaaatttt tgtggatgga 300
 gatagccttt ttgaatattt acatgctcaa acatttcctt ctaatataga aaatctacaa 360
 ctaacgaatt cattaaatga tgctttaaga aataataata aagtctatac ttttttttct 420
 acaaaccttg ttgaaaaagc taatacagtt gtaggtgctt cactttttgt aaactgggta 480
 aaaggagtaa tagatgattt tacatctgaa tccacacaaa aaagtactat agataaagtt 540
 tcagatgtat ccataattat tccctatata ggacctgctt tgaatgtagg aaatgaaaca 600

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gctaaagaaa attttaaaaa tgcttttgaa ataggtggag ccgctatctt aatggagttt 660
attccagaac ttattgtacc tatagttgga ttttttacat tagaatcata tgtaggaaat 720
aaagggcata ttattatgac gatatccaat gctttaaaga aaagggatca aaaatggaca 780
gatatgtatg gtttgatagt atcgcagtgg ctctcaacgg ttaatactca attttataca 840
ataaaagaaa gaatgtacaa tgcttttaaat aatcaatcac aagcaataga aaaaataata 900
gaagatcaat ataatagata tagtgaagaa gataaaatga atattaacat tgatttttaat 960
gatatagatt ttaaacttaa tcaaagtata aatntagcaa taaacaatat agatgatttt 1020
ataaaccaat gttctatata atatctaata aatagaatga ttccattagc tgtaaaaaag 1080
ttaaaagact ttgatgataa tcttaagaga gattttattgg agtatataga tacaaatgaa 1140
ctatatttac ttgatgaagt aaatattcta aaatcaaaaag taaatagaca cctaaaagac 1200
agtataccat ttgatctttc actatatacc taa                                     1233

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<210> 32

<211> 410

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTG Hn

<400> 32

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Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn
 1           5           10           15
Glu Asp Leu Phe Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu
          20           25           30
Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu
          35           40           45
Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser
          50           55           60
Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp
65           70           75           80
Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Lys Ile
          85           90           95
Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe
          100          105          110
Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala
          115          120          125
Leu Arg Asn Asn Asn Lys Val Tyr Thr Phe Phe Ser Thr Asn Leu Val
          130          135          140
Glu Lys Ala Asn Thr Val Val Gly Ala Ser Leu Phe Val Asn Trp Val
145          150          155          160
Lys Gly Val Ile Asp Asp Phe Thr Ser Glu Ser Thr Gln Lys Ser Thr
          165          170          175
Ile Asp Lys Val Ser Asp Val Ser Ile Ile Ile Pro Tyr Ile Gly Pro
          180          185          190
Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Glu Asn Phe Lys Asn Ala
          195          200          205
Phe Glu Ile Gly Gly Ala Ala Ile Leu Met Glu Phe Ile Pro Glu Leu
          210          215          220
Ile Val Pro Ile Val Gly Phe Phe Thr Leu Glu Ser Tyr Val Gly Asn
225          230          235          240
Lys Gly His Ile Ile Met Thr Ile Ser Asn Ala Leu Lys Lys Arg Asp
          245          250          255
Gln Lys Trp Thr Asp Met Tyr Gly Leu Ile Val Ser Gln Trp Leu Ser
          260          265          270
Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Arg Met Tyr Asn Ala

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	275		280		285	
Leu	Asn Asn Gln Ser Gln Ala	Ile Glu Lys Ile	Ile Glu Asp Gln Tyr			
290		295	300			
Asn Arg Tyr Ser Glu Glu Asp Lys Met Asn Ile	Asn Ile Asp Phe Asn					
305		310	315		320	
Asp Ile Asp Phe Lys Leu Asn Gln Ser Ile Asn Leu Ala Ile	Asn Asn					
	325		330		335	
Ile Asp Asp Phe Ile Asn Gln Cys Ser Ile Ser Tyr Leu Met Asn Arg						
	340		345		350	
Met Ile Pro Leu Ala Val Lys Lys Leu Lys Asp Phe Asp Asp Asn Leu						
	355		360		365	
Lys Arg Asp Leu Leu Glu Tyr Ile Asp Thr Asn Glu Leu Tyr Leu Leu						
	370		375		380	
Asp Glu Val Asn Ile Leu Lys Ser Lys Val Asn Arg His Leu Lys Asp						
385		390	395		400	
Ser Ile Pro Phe Asp Leu Ser Leu Tyr Thr						
	405		410			

<210> 33
 <211> 1314
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTF Hc

<400> 33
 gaattcacga tgtcttacac taacgacaaa atcctgatcc tgtacttcaa caaactgtac 60
 aaaaaaatca aagacaactc tatcctggac atgcgttacg aaaacaacaa attcatcgac 120
 atctctggct atgggttctaa catctctatc aacggtgacg tctacatcta ctctactaac 180
 cgcaaccagt tcggtatcta ctcttctaaa ccgtctgaag taaacatcgc tcagaacaac 240
 gacatcatct acaacggtcg ttaccagaac ttctctatct ctttctgggt tcgtatcccg 300
 aaatacttca acaaagttaa cctgaacaac gaatacacta tcatcgactg catccgtaac 360
 aacaactctg gttggaaaat ctctctgaac tacaacaaaa tcatctggac tctgcaggac 420
 actgctggta acaaccagaa actgggtttc aactacactc agatgatctc tatctctgac 480
 tacattaata aatggatctt cgttactatc actaacaacc gtctgggtaa ctctcgtatc 540
 tacatcaacg gtaacctgat cgatgaaaaa tctatctcta acctgggtga catccacggt 600
 tctgacaaca tcctgttcaa aatcgttggt tgcaacgaca cgcggttacgt tggatatccgt 660
 tacttcaaag ttttcgacac tgaactgggt aaaactgaaa tcgaaactct gtactctgac 720
 gaaccggacc cgtctatcct gaaagacttc tggggtaact acctgctgta caacaaacgt 780
 tactacctgc tgaacctgct ccggactgac aaatctatca ctcagaactc taacttcctg 840
 aacatcaacc agcagcgtgg tgtttatcag aaacctaata tcttctctaa cactcgtctg 900
 tacactgggtg ttgaagttat catccgtaaa aacggttcta ctgacatctc taacactgac 960
 aacttcgtac gtaaaaacga cctggcttac atcaacggtg ttgaccgtga cgttgaatac 1020
 cgtctgtacg ctgacatctc tatcgctaaa ccggaaaaaa tcatcaaact gatccgtact 1080
 tctaactcta acaactctct gggtcagatc atcgttatgg actcgatcgg taacaactgc 1140
 actatgaact tccagaacaa caacggtgggt aacatcgggtc tgctggggtt ccactctaac 1200
 aacctgggtg cttcttcatg gtactacaac aacatccgta aaaacacttc ttctaacggt 1260
 tgcttctgggt ctttcatctc taaagaacac ggttggcagg aaaactaaga attc 1314

<210> 34
 <211> 432
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTF Hc

<400> 34

Met	Ser	Tyr	Thr	Asn	Asp	Lys	Ile	Leu	Ile	Leu	Tyr	Phe	Asn	Lys	Leu
1				5				10						15	
Tyr	Lys	Lys	Ile	Lys	Asp	Asn	Ser	Ile	Leu	Asp	Met	Arg	Tyr	Glu	Asn
			20					25					30		
Asn	Lys	Phe	Ile	Asp	Ile	Ser	Gly	Tyr	Gly	Ser	Asn	Ile	Ser	Ile	Asn
		35					40					45			
Gly	Asp	Val	Tyr	Ile	Tyr	Ser	Thr	Asn	Arg	Asn	Gln	Phe	Gly	Ile	Tyr
	50					55					60				
Ser	Ser	Lys	Pro	Ser	Glu	Val	Asn	Ile	Ala	Gln	Asn	Asn	Asp	Ile	Ile
65					70					75					80
Tyr	Asn	Gly	Arg	Tyr	Gln	Asn	Phe	Ser	Ile	Ser	Phe	Trp	Val	Arg	Ile
				85					90					95	
Pro	Lys	Tyr	Phe	Asn	Lys	Val	Asn	Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile
			100					105					110		
Asp	Cys	Ile	Arg	Asn	Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser	Leu	Asn	Tyr
		115					120					125			
Asn	Lys	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Ala	Gly	Asn	Asn	Gln	Lys
		130				135					140				
Leu	Val	Phe	Asn	Tyr	Thr	Gln	Met	Ile	Ser	Ile	Ser	Asp	Tyr	Ile	Asn
145					150					155					160
Lys	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Gly	Asn	Ser	Arg
			165						170					175	
Ile	Tyr	Ile	Asn	Gly	Asn	Leu	Ile	Asp	Glu	Lys	Ser	Ile	Ser	Asn	Leu
			180					185					190		
Gly	Asp	Ile	His	Val	Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile	Val	Gly	Cys
		195					200					205			
Asn	Asp	Thr	Arg	Tyr	Val	Gly	Ile	Arg	Tyr	Phe	Lys	Val	Phe	Asp	Thr
		210				215					220				
Glu	Leu	Gly	Lys	Thr	Glu	Ile	Glu	Thr	Leu	Tyr	Ser	Asp	Glu	Pro	Asp
225					230					235					240
Pro	Ser	Ile	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr	Asn	Lys
				245					250					255	
Arg	Tyr	Tyr	Leu	Leu	Asn	Leu	Leu	Arg	Thr	Asp	Lys	Ser	Ile	Thr	Gln
			260					265					270		
Asn	Ser	Asn	Phe	Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val	Tyr	Gln	Lys
		275					280					285			
Pro	Asn	Ile	Phe	Ser	Asn	Thr	Arg	Leu	Tyr	Thr	Gly	Val	Glu	Val	Ile
		290				295					300				
Ile	Arg	Lys	Asn	Gly	Ser	Thr	Asp	Ile	Ser	Asn	Thr	Asp	Asn	Phe	Val
305				310						315					320
Arg	Lys	Asn	Asp	Leu	Ala	Tyr	Ile	Asn	Val	Val	Asp	Arg	Asp	Val	Glu
			325						330					335	
Tyr	Arg	Leu	Tyr	Ala	Asp	Ile	Ser	Ile	Ala	Lys	Pro	Glu	Lys	Ile	Ile
			340					345					350		
Lys	Leu	Ile	Arg	Thr	Ser	Asn	Ser	Asn	Asn	Ser	Leu	Gly	Gln	Ile	Ile
		355					360					365			
Val	Met	Asp	Ser	Ile	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe	Gln	Asn	Asn
		370				375					380				
Asn	Gly	Gly	Asn	Ile	Gly	Leu	Leu	Gly	Phe	His	Ser	Asn	Asn	Leu	Val
385					390					395					400
Ala	Ser	Ser	Trp	Tyr	Tyr	Asn	Asn	Ile	Arg	Lys	Asn	Thr	Ser	Ser	Asn
			405						410					415	
Gly	Cys	Phe	Trp	Ser	Phe	Ile	Ser	Lys	Glu	His	Gly	Trp	Gln	Glu	Asn

420

425

430

<210> 35
 <211> 1278
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTE Hc

<400> 35
 ttcgaaacga tgattttaat ttctacttc aacaagttct tcaagagaat taagtcttct 60
 tccgttttaa acatgagata caagaatgat aaatacgtcg acacttccgg ttacgactcc 120
 aatatcaaca ttaacggtga cgtgtacaag taccacaacta acaaaaacca attcgggtatc 180
 tacaacgaca agcttactga gctgaacatc tctcaaaacg actacattat ctacgacaac 240
 aagtacaata acttctctat ttctttctgg gtcagaattc ctaactacga taacaagatc 300
 gtcaacgtta acaacgagta cactatcatc aactgtatga gagacaacaa ctccgggttg 360
 aaggtctctc ttaaccacaa cgagatgatt tggaccttgc aagacaacgc aggtattaac 420
 caaaagttag cattcaacta cggtaacgca aacgggtattt ctgactacat caacaagtgg 480
 attttcgtca ctatcactaa cgacagatta ggggactcta agctttacat taacggtaac 540
 ttaatcgacc aaaagtccat tttaaactta ggtaacattc acgtttctga caacatctta 600
 ttcaagatcg ttaactgcag ttacaacaga tacattggca ttagatactt caacattttc 660
 gacaaggagt tagacgagac cgagattcaa actttatata gcaacgaacc taacaccaat 720
 attttgaagg acttctgggg taactacttg ctttacgaca aggaatacta cttattaaac 780
 gtgttaaagc caaacaactt cattgatagg agaaaggatt ctactttaag cattaacaac 840
 atcagaagca ctattctttt agctaacaga ttatactctg gtatcaagggt taagatccaa 900
 agagttaaca actcttctac taacgataac cttgttagaa agaacgatca ggtctatatt 960
 aacttcgtcg ctagcaagac tcacttattc ccatttatat ctgataacgc taccaccaac 1020
 aaggagaaga ccatcaagat ctctctctct ggcaacagat ttaaccaagt cgtcgttatg 1080
 aactccgtcg gtaacaactg taccatgaac tttaaaaata ataattggaa taatattggg 1140
 tgtttagggt tcaaggcaga tactgtagtt gctagtactt ggtattatac ccacatgaga 1200
 gatcacacca acagcaatgg atgtttttgg aactttattt ctgaagaaca tggatggcaa 1260
 gaaaaataat agggatcc 1278

<210> 36
 <211> 419
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Encoded polypeptide of a synthetic construct based
 on BoNTE Hc

<400> 36
 Met Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser
 1 5 10 15
 Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr
 20 25 30
 Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr
 35 40 45
 Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Thr Glu
 50 55 60
 Leu Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys
 65 70 75 80
 Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys
 85 90 95

Ile	Val	Asn	Val	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Arg	Asp	
			100					105					110			
Asn	Asn	Ser	Gly	Trp	Lys	Val	Ser	Leu	Asn	His	Asn	Glu	Ile	Ile	Trp	
		115					120					125				
Thr	Leu	Gln	Asp	Asn	Ala	Gly	Ile	Asn	Gln	Lys	Leu	Ala	Phe	Asn	Tyr	
	130					135					140					
Gly	Asn	Ala	Asn	Gly	Ile	Ser	Asp	Tyr	Ile	Asn	Lys	Trp	Ile	Phe	Val	
145					150					155					160	
Thr	Ile	Thr	Asn	Asp	Arg	Leu	Gly	Asp	Ser	Lys	Leu	Tyr	Ile	Asn	Gly	
			165					170						175		
Asn	Leu	Ile	Asp	Gln	Lys	Ser	Ile	Leu	Asn	Leu	Gly	Asn	Ile	His	Val	
		180						185					190			
Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile	Val	Asn	Cys	Ser	Tyr	Thr	Arg	Tyr	
	195						200					205				
Ile	Gly	Ile	Arg	Tyr	Phe	Asn	Ile	Phe	Asp	Lys	Glu	Leu	Asp	Glu	Thr	
	210					215					220					
Glu	Ile	Gln	Thr	Leu	Tyr	Ser	Asn	Glu	Pro	Asn	Thr	Asn	Ile	Leu	Lys	
225					230					235					240	
Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr	Asp	Lys	Glu	Tyr	Tyr	Leu	Leu	
			245					250						255		
Asn	Val	Leu	Lys	Pro	Asn	Asn	Phe	Ile	Asp	Arg	Arg	Lys	Asp	Ser	Thr	
		260					265						270			
Leu	Ser	Ile	Asn	Asn	Ile	Arg	Ser	Thr	Ile	Leu	Leu	Ala	Asn	Arg	Leu	
	275					280						285				
Tyr	Ser	Gly	Ile	Lys	Val	Lys	Ile	Gln	Arg	Val	Asn	Asn	Ser	Ser	Thr	
	290					295					300					
Asn	Asp	Asn	Leu	Val	Arg	Lys	Asn	Asp	Gln	Val	Tyr	Ile	Asn	Phe	Val	
305					310				315						320	
Ala	Ser	Lys	Thr	His	Leu	Phe	Pro	Leu	Tyr	Ala	Asp	Thr	Ala	Thr	Thr	
			325					330						335		
Asn	Lys	Glu	Lys	Thr	Ile	Lys	Ile	Ser	Ser	Ser	Gly	Asn	Arg	Phe	Asn	
		340						345					350			
Gln	Val	Val	Val	Met	Asn	Ser	Val	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe	
	355						360					365				
Lys	Asn	Asn	Asn	Gly	Asn	Asn	Ile	Gly	Leu	Leu	Gly	Phe	Lys	Ala	Asp	
	370					375					380					
Thr	Val	Val	Ala	Ser	Thr	Trp	Tyr	Tyr	Thr	His	Met	Arg	Asp	His	Thr	
385					390					395					400	
Asn	Ser	Asn	Gly	Cys	Phe	Trp	Asn	Phe	Ile	Ser	Glu	Glu	His	Gly	Trp	
			405					410						415		
Gln	Glu	Lys														

<210> 37

<211> 1338

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTA Hc

<400> 37

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ctcgagccat ggctcgctctg ctgtctacct tcaactgaata catcaagaac atcatcaata 60
cctccatcct gaacctgcgc tacgaatcca atcacctgat cgacctgtct cgctacgctt 120
ccaaaatcaa catcggttct aaagttaact tcgatccgat cgacaagaat cagatccagc 180
tgttcaatct ggaatcttcc aaaatcgaag ttatcctgaa gaatgctatc gtatacaact 240

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ctatgtacga aaactttctcc acctccttct ggatccgtat cccgaaatac ttcaactcca 300
tctctctgaa caatgaatac accatcatca actgcatgga aaacaattct gggtggaaag 360
tatctctgaa ctacggtgaa atcatctgga ctctgcagga cactcaggaa atcaaacagc 420
gtgttgattt caaatactct cagatgatca acatctctga ctacatcaat cgctggatct 480
tcgttaccat caccaacaat cgtctgaata actccaaaat ctacatcaac ggccgtctga 540
tcgaccagaa accgatctcc aatctgggta acatccacgc ttctaataac atcatgttca 600
aactggacgg ttgtcgtgac actcacgcgt acatctggat caaatacttc aatctgttcg 660
acaaagaact gaacgaaaaa gaaatcaaag acctgtacga caaccagtcc aattctggta 720
tcctgaaaga cttctgggggt gactacctgc agtacgacaa accgtactac atgctgaatc 780
tgtacgatcc gaacaaatac gttgacgtca acaatgtagg tatccgcggt tacatgtacc 840
tgaaagggtcc gcgtgggttct gttatgacta ccaacatcta cctgaactct tccctgtacc 900
gtggtaccaa attcatcatc aagaaatacg cgtctggtaa caaggacaat atcggttcga 960
acaatgatcg tgtatacatc aatggttag ttaagaacaa agaataccgt ctgggtacca 1020
atgcttctca ggctgggtga gaaaagatct tgtctgctct ggaaatcccg gacgttggtg 1080
atctgtctca ggtagttgta atgaaatcca agaacgacca gggtatcact aacaaatgca 1140
aaatgaatct gcaggacaac aatggtaacg atatcggttt catcggtttc caccagttca 1200
acaatatcgc taaactgggt gcttccaact ggtacaatcg tcagatcgaa cgttcctctc 1260
gcactctggg ttgctcttgg gagttcatcc cggttgatga cggttggggg gaacgtccgc 1320
tgtaaccgga gaaagctt                                     1338

```

<210> 38

<211> 415

<212> PRT

<213> Clostridium botulinum

<400> 38

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Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys
1           5           10           15
Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln
20           25           30
Ile Gln Leu Phe Asn Leu Glu Ser Lys Ile Glu Val Ile Leu Lys
35           40           45
Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe
50           55           60
Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu
65           70           75           80
Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser
85           90           95
Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile
100          105          110
Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp
115          120          125
Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn
130          135          140
Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile
145          150          155          160
Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu
165          170          175
Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Phe Tyr Phe Asn
180          185          190
Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp
195          200          205
Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu
210          215          220
Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys
225          230          235          240
Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys

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				245					250				255				
Gly	Pro	Arg	Gly	Ser	Val	Met	Thr	Thr	Asn	Ile	Tyr	Leu	Asn	Ser	Ser		
			260						265				270				
Leu	Tyr	Arg	Gly	Thr	Lys	Phe	Ile	Ile	Lys	Lys	Tyr	Ala	Ser	Gly	Asn		
		275					280					285					
Lys	Asp	Asn	Ile	Val	Arg	Asn	Asn	Asp	Arg	Val	Tyr	Ile	Asn	Val	Val		
	290					295					300						
Val	Lys	Asn	Lys	Glu	Tyr	Arg	Leu	Ala	Thr	Asn	Ala	Ser	Gln	Ala	Gly		
305					310					315					320		
Val	Glu	Lys	Ile	Leu	Ser	Ala	Leu	Glu	Ile	Pro	Asp	Val	Gly	Asn	Leu		
			325						330					335			
Ser	Gln	Val	Val	Val	Met	Lys	Ser	Lys	Asn	Asp	Gln	Gly	Ile	Thr	Asn		
		340						345					350				
Lys	Cys	Lys	Met	Asn	Leu	Gln	Asp	Asn	Asn	Gly	Asn	Asp	Ile	Gly	Phe		
	355					360						365					
Ile	Gly	Phe	His	Gln	Phe	Asn	Asn	Ile	Ala	Lys	Leu	Val	Ala	Ser	Asn		
	370					375					380						
Trp	Tyr	Asn	Arg	Gln	Ile	Glu	Arg	Ser	Ser	Arg	Thr	Leu	Gly	Cys	Ser		
385				390					395						400		
Trp	Glu	Phe	Ile	Pro	Val	Asp	Asp	Gly	Trp	Gly	Glu	Arg	Pro	Leu			
			405					410						415			

<210> 39
 <211> 1351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTB Hc

<400> 39
 atggctttca acaaatacaa ttccgaaatc ctgaacaata tcatcctgaa cctgcgttac 60
 aaagacaaca atctgatcga tctgtctggt tacgggtgcta aagttgaagt atacgacggt 120
 gttgaactga atgacaagaa ccagttcaaa ctgacctctt ccgctaactc taagatccgt 180
 gttactcaga atcagaacat catcttcaac tccgtattcc tggacttctc tgtttccttc 240
 tggatccgta tcccgaata caagaacgac ggtatccaga attacatcca caatgaatac 300
 accatcatca actgcatgaa gaataactct ggttggaaga tctccatccg cggtaacggt 360
 atcatctgga ctctgatcga tatcaacggt aagaccaaat ctgtattctt cgaatacaac 420
 atccgtgaag acatctctga atacatcaat cgctggttct tcgttaccat caccaataac 480
 ctgaacaatg ctaaaatcta catcaacggt aaactggaat ctaataccga catcaaagac 540
 atccgtgaag ttatcgctaa cggtgaaatc atcttcaaac tggacggtga catcgatcgt 600
 acccagttca tctggatgaa atacttctcc atcttcaaca ccgaactgtc tcagtccaat 660
 atcgaagaac ggtacaagat ccagtcttac tccgaatacc tgaaagactt ctggggtaat 720
 ccgctgatgt acaacaaaga atactatatg ttcaatgctg gtaacaagaa ctcttacatc 780
 aaactgaaga aagactctcc ggttggtgaa atcctgactc gttccaaata caaccagaac 840
 tctaaatata tcaactaccg cgacctgtac atcggtgaaa agttcatcat ccgtcgcaaa 900
 tctaactctc agtccatcaa tgatgacatc gtacgtaaag aagactacat ctacctggac 960
 ttcttcaacc tgaatcagga atggcgtgta tacacctaca agtacttcaa gaaagaagaa 1020
 gaaaagcttt tcttggctcc gatctctgat tccgacgaac tctacaacac catccagatc 1080
 aaagaatacg acgaacagcc gacctactct tgccagctgc tgttcaagaa agatgaagaa 1140
 tctactgacg aaatcgggtc gatcgggtatc caccgtttct acgaatctgg tatcgtattc 1200
 gaagaatata aagactactt ctgcatctcc aaatggtacc tgaagggaagt taaacgcaaa 1260
 ccgtacaacc tgaaactggg ttgcaattgg cagttcatcc cgaaagacga aggttggacc 1320
 gaatagtaac ctctagatc gaggcctgca g 1351

<210> 40

<211> 439
 <212> PRT
 <213> Clostridium botulinum

<400> 40

Phe	Asn	Lys	Tyr	Asn	Ser	Glu	Ile	Leu	Asn	Asn	Ile	Ile	Leu	Asn	Leu	1	5	10	15
Arg	Tyr	Lys	Asp	Asn	Asn	Leu	Ile	Asp	Leu	Ser	Gly	Tyr	Gly	Ala	Lys	20	25	30	
Val	Glu	Val	Tyr	Asp	Gly	Val	Glu	Leu	Asn	Asp	Lys	Asn	Gln	Phe	Lys	35	40	45	
Leu	Thr	Ser	Ser	Ala	Asn	Ser	Lys	Ile	Arg	Val	Thr	Gln	Asn	Gln	Asn	50	55	60	
Ile	Ile	Phe	Asn	Ser	Val	Phe	Leu	Asp	Phe	Ser	Val	Ser	Phe	Trp	Ile	65	70	75	80
Arg	Ile	Pro	Lys	Tyr	Lys	Asn	Asp	Gly	Ile	Gln	Asn	Tyr	Ile	His	Asn	85	90	95	
Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Lys	Asn	Asn	Ser	Gly	Trp	Lys	Ile	100	105	110	
Ser	Ile	Arg	Gly	Asn	Arg	Ile	Ile	Trp	Thr	Leu	Ile	Asp	Ile	Asn	Gly	115	120	125	
Lys	Thr	Lys	Ser	Val	Phe	Phe	Glu	Tyr	Asn	Ile	Arg	Glu	Asp	Ile	Ser	130	135	140	
Glu	Tyr	Ile	Asn	Arg	Trp	Phe	Phe	Val	Thr	Ile	Thr	Asn	Asn	Leu	Asn	145	150	155	160
Asn	Ala	Lys	Ile	Tyr	Ile	Asn	Gly	Lys	Leu	Glu	Ser	Asn	Thr	Asp	Ile	165	170	175	
Lys	Asp	Ile	Arg	Glu	Val	Ile	Ala	Asn	Gly	Glu	Ile	Ile	Phe	Lys	Leu	180	185	190	
Asp	Gly	Asp	Ile	Asp	Arg	Thr	Gln	Phe	Ile	Trp	Met	Lys	Tyr	Phe	Ser	195	200	205	
Ile	Phe	Asn	Thr	Glu	Leu	Ser	Gln	Ser	Asn	Ile	Glu	Glu	Arg	Tyr	Lys	210	215	220	
Ile	Gln	Ser	Tyr	Ser	Glu	Tyr	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Pro	Leu	225	230	235	240
Met	Tyr	Asn	Lys	Glu	Tyr	Tyr	Met	Phe	Asn	Ala	Gly	Asn	Lys	Asn	Ser	245	250	255	
Tyr	Ile	Lys	Leu	Lys	Lys	Asp	Ser	Pro	Val	Gly	Glu	Ile	Leu	Thr	Arg	260	265	270	
Ser	Lys	Tyr	Asn	Gln	Asn	Ser	Lys	Tyr	Ile	Asn	Tyr	Arg	Asp	Leu	Tyr	275	280	285	
Ile	Gly	Glu	Lys	Phe	Ile	Ile	Arg	Arg	Lys	Ser	Asn	Ser	Gln	Ser	Ile	290	295	300	
Asn	Asp	Asp	Ile	Val	Arg	Lys	Glu	Asp	Tyr	Ile	Tyr	Leu	Asp	Phe	Phe	305	310	315	320
Asn	Leu	Asn	Gln	Glu	Trp	Arg	Val	Tyr	Thr	Tyr	Lys	Tyr	Phe	Lys	Lys	325	330	335	
Glu	Glu	Glu	Lys	Leu	Phe	Leu	Ala	Pro	Ile	Ser	Asp	Ser	Asp	Glu	Phe	340	345	350	
Tyr	Asn	Thr	Ile	Gln	Ile	Lys	Glu	Tyr	Asp	Glu	Gln	Pro	Thr	Tyr	Ser	355	360	365	
Cys	Gln	Leu	Leu	Phe	Lys	Lys	Asp	Glu	Glu	Ser	Thr	Asp	Glu	Ile	Gly	370	375	380	
Leu	Ile	Gly	Ile	His	Arg	Phe	Tyr	Glu	Ser	Gly	Ile	Val	Phe	Glu	Glu	385	390	395	400
Tyr	Lys	Asp	Tyr	Phe	Cys	Ile	Ser	Lys	Trp	Tyr	Leu	Lys	Glu	Val	Lys	405	410	415	

Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile Pro
 420 425 430
 Lys Asp Glu Gly Trp Thr Glu
 435

<210> 41
 <211> 848
 <212> PRT
 <213> Clostridium botulinum

<400> 41
 Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
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 Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu
 20 25 30
 Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
 35 40 45
 Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro
 50 55 60
 Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
 65 70 75 80
 Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
 85 90 95
 Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu
 100 105 110
 His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu
 115 120 125
 Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys
 130 135 140
 Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu
 145 150 155 160
 Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr
 165 170 175
 Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala
 180 185 190
 Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu
 195 200 205
 Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala
 210 215 220
 Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys
 225 230 235 240
 Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu
 245 250 255
 Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys
 260 265 270
 Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu
 275 280 285
 Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn
 290 295 300
 Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp
 305 310 315 320
 Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile
 325 330 335
 Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met
 340 345 350
 Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys

		355					360					365				
Asp	Ala	Leu	Leu	Lys	Tyr	Ile	Tyr	Asp	Asn	Arg	Gly	Thr	Leu	Ile	Gly	
	370					375					380					
Gln	Val	Asp	Arg	Leu	Lys	Asp	Lys	Val	Asn	Asn	Thr	Leu	Ser	Thr	Asp	
385					390					395					400	
Ile	Pro	Phe	Gln	Leu	Ser	Lys	Tyr	Val	Asp	Asn	Gln	Arg	Leu	Leu	Ser	
				405					410					415		
Thr	Phe	Thr	Glu	Tyr	Ile	Lys	Asn	Ile	Ile	Asn	Thr	Ser	Ile	Leu	Asn	
			420					425					430			
Leu	Arg	Tyr	Glu	Ser	Asn	His	Leu	Ile	Asp	Leu	Ser	Arg	Tyr	Ala	Ser	
		435					440					445				
Lys	Ile	Asn	Ile	Gly	Ser	Lys	Val	Asn	Phe	Asp	Pro	Ile	Asp	Lys	Asn	
	450					455					460					
Gln	Ile	Gln	Leu	Phe	Asn	Leu	Glu	Ser	Ser	Lys	Ile	Glu	Val	Ile	Leu	
465					470					475					480	
Lys	Asn	Ala	Ile	Val	Tyr	Asn	Ser	Met	Tyr	Glu	Asn	Phe	Ser	Thr	Ser	
				485					490					495		
Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Ser	Ile	Ser	Leu	Asn	Asn	
			500					505					510			
Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Glu	Asn	Asn	Ser	Gly	Trp	Lys	Val	
		515				520						525				
Ser	Leu	Asn	Tyr	Gly	Glu	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Gln	Glu	
	530					535					540					
Ile	Lys	Gln	Arg	Val	Val	Phe	Lys	Tyr	Ser	Gln	Met	Ile	Asn	Ile	Ser	
545					550					555					560	
Asp	Tyr	Ile	Asn	Arg	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	
				565					570					575		
Asn	Asn	Ser	Lys	Ile	Tyr	Ile	Asn	Gly	Arg	Leu	Ile	Asp	Gln	Lys	Pro	
			580					585					590			
Ile	Ser	Asn	Leu	Gly	Asn	Ile	His	Ala	Ser	Asn	Asn	Ile	Met	Phe	Lys	
		595					600						605			
Leu	Asp	Gly	Cys	Arg	Asp	Thr	His	Arg	Tyr	Ile	Trp	Ile	Lys	Tyr	Phe	
	610					615					620					
Asn	Leu	Phe	Asp	Lys	Glu	Leu	Asn	Glu	Lys	Glu	Ile	Lys	Asp	Leu	Tyr	
625					630					635					640	
Asp	Asn	Gln	Ser	Asn	Ser	Gly	Ile	Leu	Lys	Asp	Phe	Trp	Gly	Asp	Tyr	
				645					650					655		
Leu	Gln	Tyr	Asp	Lys	Pro	Tyr	Tyr	Met	Leu	Asn	Leu	Tyr	Asp	Pro	Asn	
			660					665					670			
Lys	Tyr	Val	Asp	Val	Asn	Asn	Val	Gly	Ile	Arg	Gly	Tyr	Met	Tyr	Leu	
		675					680					685				
Lys	Gly	Pro	Arg	Gly	Ser	Val	Met	Thr	Thr	Asn	Ile	Tyr	Leu	Asn	Ser	
	690					695					700					
Ser	Leu	Tyr	Arg	Gly	Thr	Lys	Phe	Ile	Ile	Lys	Lys	Tyr	Ala	Ser	Gly	
705					710											

Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys
820 825 830
Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu
835 840 845

<210> 42
<211> 850
<212> PRT
<213> Clostridium botulinum

<400> 42
Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe Ile
1 5 10 15
Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg Ile
20 25 30
Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile Asn
35 40 45
Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro Ser
50 55 60
Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val Tyr
65 70 75 80
Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr Ile
85 90 95
Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp Ile
100 105 110
Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys Val
115 120 125
Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val Val
130 135 140
Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp Phe
145 150 155 160
Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp Ile
165 170 175
Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn Glu
180 185 190
Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala Ser
195 200 205
Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly Ala
210 215 220
Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys Thr
225 230 235 240
Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met Tyr
245 250 255
Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe Tyr
260 265 270
Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln Ala
275 280 285
Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys Glu
290 295 300
Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu Asn
305 310 315 320
Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn Gly
325 330 335
Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val Glu
340 345 350
Lys Leu Leu Asp Phe Asp Asn Thr Leu Lys Lys Asn Leu Leu Asn Tyr

		355					360					365				
Ile	Asp	Glu	Asn	Lys	Leu	Tyr	Leu	Ile	Gly	Ser	Ala	Glu	Tyr	Glu	Lys	
	370					375					380					
Ser	Lys	Val	Asn	Lys	Tyr	Leu	Lys	Thr	Ile	Met	Pro	Phe	Asp	Leu	Ser	
385					390					395					400	
Ile	Tyr	Thr	Asn	Asp	Thr	Ile	Leu	Ile	Glu	Met	Phe	Asn	Lys	Tyr	Asn	
				405					410					415		
Ser	Glu	Ile	Leu	Asn	Asn	Ile	Ile	Leu	Asn	Leu	Arg	Tyr	Lys	Asp	Asn	
				420				425					430			
Asn	Leu	Ile	Asp	Leu	Ser	Gly	Tyr	Gly	Ala	Lys	Val	Glu	Val	Tyr	Asp	
		435				440						445				
Gly	Val	Glu	Leu	Asn	Asp	Lys	Asn	Gln	Phe	Lys	Leu	Thr	Ser	Ser	Ala	
	450					455					460					
Asn	Ser	Lys	Ile	Arg	Val	Thr	Gln	Asn	Gln	Asn	Ile	Ile	Phe	Asn	Ser	
465					470					475					480	
Val	Phe	Leu	Asp	Phe	Ser	Val	Ser	Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	
				485					490					495		
Lys	Asn	Asp	Gly	Ile	Gln	Asn	Tyr	Ile	His	Asn	Glu	Tyr	Thr	Ile	Ile	
			500					505					510			
Asn	Cys	Met	Lys	Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser	Ile	Arg	Gly	Asn	
		515					520					525				
Arg	Ile	Ile	Trp	Thr	Leu	Ile	Asp	Ile	Asn	Gly	Lys	Thr	Lys	Ser	Val	
	530					535					540					
Phe	Phe	Glu	Tyr	Asn	Ile	Arg	Glu	Asp	Ile	Ser	Glu	Tyr	Ile	Asn	Arg	
545					550					555					560	
Trp	Phe	Phe	Val	Thr	Ile	Thr	Asn	Asn	Leu	Asn	Asn	Ala	Lys	Ile	Tyr	
				565					570					575		
Ile	Asn	Gly	Lys	Leu	Glu	Ser	Asn	Thr	Asp	Ile	Lys	Asp	Ile	Arg	Glu	
			580					585					590			
Val	Ile	Ala	Asn	Gly	Glu	Ile	Ile	Phe	Lys	Leu	Asp	Gly	Asp	Ile	Asp	
		595					600					605				
Arg	Thr	Gln	Phe	Ile	Trp	Met	Lys	Tyr	Phe	Ser	Ile	Phe	Asn	Thr	Glu	
	610					615					620					
Leu	Ser	Gln	Ser	Asn	Ile	Glu	Glu	Arg	Tyr	Lys	Ile	Gln	Ser	Tyr	Ser	
625					630					635					640	
Glu	Tyr	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Pro	Leu	Met	Tyr	Asn	Lys	Glu	
				645					650					655		
Tyr	Tyr	Met	Phe	Asn	Ala	Gly	Asn	Lys	Asn	Ser	Tyr	Ile	Lys	Leu	Lys	
			660					665					670			
Lys	Asp	Ser	Pro	Val	Gly	Glu	Ile	Leu	Thr	Arg	Ser	Lys	Tyr	Asn	Gln	
		675					680					685				
Asn	Ser	Lys	Tyr	Ile	Asn	Tyr	Arg	Asp	Leu	Tyr	Ile	Gly	Glu	Lys	Phe	
		690				695					700					
Ile	Ile	Arg	Arg	Lys	Ser	Asn	Ser	Gln	Ser	Ile	Asn	Asp	Asp	Ile	Val	
705					710											

Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val Lys Arg Lys Pro Tyr Asn
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 Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile Pro Lys Asp Glu Gly Trp
 835 840 845
 Thr Glu
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 Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Val Gly Gln Met Gln Pro
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 Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
 35 40 45
 Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
 50 55 60
 Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
 65 70 75 80
 Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
 85 90 95
 Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
 100 105 110
 Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
 115 120 125
 Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
 130 135 140
 Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile
 145 150 155 160
 Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr
 165 170 175
 Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
 180 185 190
 Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
 195 200 205
 Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
 210 215 220
 Leu Ile His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
 225 230 235 240
 Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
 245 250 255
 Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
 260 265 270
 Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
 275 280 285
 Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
 290 295 300
 Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys

305					310					315				320
Tyr	Leu	Leu	Ser	Glu	Asp	Thr	Ser	Gly	Lys	Phe	Ser	Val	Asp	Lys
				325					330					335
Lys	Phe	Asp	Lys	Leu	Tyr	Lys	Met	Leu	Thr	Glu	Ile	Tyr	Thr	Glu
			340					345					350	
Asn	Phe	Val	Lys	Phe	Phe	Lys	Val	Leu	Asn	Arg	Lys	Thr	Tyr	Leu
		355					360					365		Asn
Phe	Asp	Lys	Ala	Val	Phe	Lys	Ile	Asn	Ile	Val	Pro	Lys	Val	Asn
	370					375				380				Tyr
Thr	Ile	Tyr	Asp	Gly	Phe	Asn	Leu	Arg	Asn	Thr	Asn	Leu	Ala	Ala
385					390					395				400
Phe	Asn	Gly	Gln	Asn	Thr	Glu	Ile	Asn	Asn	Met	Asn	Phe	Thr	Lys
				405				410						415
Lys	Asn	Phe	Thr	Gly	Leu	Phe	Glu	Phe	Tyr	Lys	Leu	Leu	Cys	Val
			420					425					430	Arg
Gly	Ile	Ile	Thr	Ser	Lys	Thr	Lys	Ser	Leu	Asp	Lys	Gly	Tyr	Asn
		435					440					445		Lys
Ala	Leu	Asn	Asp	Leu	Cys	Ile	Lys	Val	Asn	Asn	Trp	Asp	Leu	Phe
	450					455				460				Phe
Ser	Pro	Ser	Glu	Asp	Asn	Phe	Thr	Asn	Asp	Leu	Asn	Lys	Gly	Glu
465					470				475					480
Ile	Thr	Ser	Asp	Thr	Asn	Ile	Glu	Ala	Ala	Glu	Glu	Asn	Ile	Ser
				485				490						495
Asp	Leu	Ile	Gln	Gln	Tyr	Tyr	Leu	Thr	Phe	Asn	Phe	Asp	Asn	Glu
		500						505					510	Pro
Glu	Asn	Ile	Ser	Ile	Glu	Asn	Leu	Ser	Ser	Asp	Ile	Ile	Gly	Gln
	515						520					525		Leu
Glu	Leu	Met	Pro	Asn	Ile	Glu	Arg	Phe	Pro	Asn	Gly	Lys	Lys	Tyr
	530				535					540				Glu
Leu	Asp	Lys	Tyr	Thr	Met	Phe	His	Tyr	Leu	Arg	Ala	Gln	Glu	Phe
545					550				555					560
His	Gly	Lys	Ser	Arg	Ile	Ala	Leu	Thr	Asn	Ser	Val	Asn	Glu	Ala
				565				570					575	Leu
Leu	Asn	Pro	Ser	Arg	Val	Tyr	Thr	Phe	Phe	Ser	Ser	Asp	Tyr	Val
		580						585					590	Lys
Lys	Val	Asn	Lys	Ala	Thr	Glu	Ala	Ala	Met	Phe	Leu	Gly	Trp	Val
	595						600					605		Glu
Gln	Leu	Val	Tyr	Asp	Phe	Thr	Asp	Glu	Thr	Ser	Glu	Val	Ser	Thr
	610					615					620			Thr
Asp	Lys	Ile	Ala	Asp	Ile	Thr	Ile	Ile	Ile	Pro	Tyr	Ile	Gly	Pro
625					630				635					640
Leu	Asn	Ile	Gly	Asn	Met	Leu	Tyr	Lys	Asp	Asp	Phe	Val	Gly	Ala
				645				650					655	Leu
Ile	Phe	Ser	Gly	Ala	Val	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Ile
	660						665					670		Ala
Ile	Pro	Val	Leu	Gly	Thr	Phe	Ala	Leu	Val	Ser	Tyr	Ile	Ala	Asn
	675					680					685			Lys
Val	Leu	Thr	Val	Gln	Thr	Ile	Asp	Asn	Ala	Leu	Ser	Lys	Arg	Asn
	690					695					700			Glu
Lys	Trp	Asp	Glu	Val	Tyr	Lys	Tyr	Ile	Val	Thr	Asn	Trp	Leu	Ala
705					710				715					720
Val	Asn	Thr	Gln	Ile	Asp	Leu	Ile	Arg	Lys	Lys	Met	Lys	Glu	Ala
				725				730					735	Leu
Glu	Asn	Gln	Ala	Glu	Ala	Thr	Lys	Ala	Ile	Ile	Asn	Tyr	Gln	Tyr
		740					745					750		Asn
Gln	Tyr	Thr	Glu	Glu	Glu	Lys	Asn	Asn	Ile	Asn	Phe	Asn	Ile	Asp
	755						760					765		Asp

Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile
 770 775 780
 Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met
 785 790 795 800
 Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys
 805 810 815
 Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly
 820 825 830
 Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp
 835 840 845
 Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser
 850 855 860
 Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn
 865 870 875 880
 Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser
 885 890 895
 Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn
 900 905 910
 Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu
 915 920 925
 Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser
 930 935 940
 Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn
 945 950 955 960
 Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val
 965 970 975
 Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu
 980 985 990
 Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser
 995 1000 1005
 Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu
 1010 1015 1020
 Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro
 1025 1030 1035 1040
 Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys
 1045 1050 1055
 Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe
 1060 1065 1070
 Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr
 1075 1080 1085
 Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr
 1090 1095 1100
 Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn
 1105 1110 1115 1120
 Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu
 1125 1130 1135
 Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser
 1140 1145 1150
 Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly
 1155 1160 1165
 Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val
 1170 1175 1180
 Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala
 1185 1190 1195 1200
 Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn
 1205 1210 1215
 Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr

1220	1225	1230
Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly		
1235	1240	1245
Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser		
1250	1255	1260
Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys		
1265	1270	1275
Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu		
1285	1290	1295

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Asn Asn Ile Ile Met Met Glu Pro Pro Phe Ala Arg Gly Thr Gly Arg		
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Tyr Tyr Lys Ala Phe Lys Ile Thr Asp Arg Ile Trp Ile Ile Pro Glu		
35	40	45
Arg Tyr Thr Phe Gly Tyr Lys Pro Glu Asp Phe Asn Lys Ser Ser Gly		
50	55	60
Ile Phe Asn Arg Asp Val Cys Glu Tyr Tyr Asp Pro Asp Tyr Leu Asn		
65	70	75
Thr Asn Asp Lys Lys Asn Ile Phe Leu Gln Thr Met Ile Lys Leu Phe		
85	90	95
Asn Arg Ile Lys Ser Lys Pro Leu Gly Glu Lys Leu Leu Glu Met Ile		
100	105	110
Ile Asn Gly Ile Pro Tyr Leu Gly Asp Arg Arg Val Pro Leu Glu Glu		
115	120	125
Phe Asn Thr Asn Ile Ala Ser Val Thr Val Asn Lys Leu Ile Ser Asn		
130	135	140
Pro Gly Glu Val Glu Arg Lys Lys Gly Ile Phe Ala Asn Leu Ile Ile		
145	150	155
Phe Gly Pro Gly Pro Val Leu Asn Glu Asn Glu Thr Ile Asp Ile Gly		
165	170	175
Ile Gln Asn His Phe Ala Ser Arg Glu Gly Phe Gly Gly Ile Met Gln		
180	185	190
Met Lys Phe Cys Pro Glu Tyr Val Ser Val Phe Asn Asn Val Gln Glu		
195	200	205
Asn Lys Gly Ala Ser Ile Phe Asn Arg Arg Gly Tyr Phe Ser Asp Pro		
210	215	220
Ala Leu Ile Leu Met His Glu Leu Ile His Val Leu His Gly Leu Tyr		
225	230	235
Gly Ile Lys Val Asp Asp Leu Pro Ile Val Pro Asn Glu Lys Lys Phe		
245	250	255
Phe Met Gln Ser Thr Asp Ala Ile Gln Ala Glu Glu Leu Tyr Thr Phe		
260	265	270
Gly Gly Gln Asp Pro Ser Ile Ile Thr Pro Ser Thr Asp Lys Ser Ile		
275	280	285

Tyr	Asp	Lys	Val	Leu	Gln	Asn	Phe	Arg	Gly	Ile	Val	Asp	Arg	Leu	Asn
290						295					300				
Lys	Val	Leu	Val	Cys	Ile	Ser	Asp	Pro	Asn	Ile	Asn	Ile	Asn	Ile	Tyr
305				310					315						320
Lys	Asn	Lys	Phe	Lys	Asp	Lys	Tyr	Lys	Phe	Val	Glu	Asp	Ser	Glu	Gly
			325						330					335	
Lys	Tyr	Ser	Ile	Asp	Val	Glu	Ser	Phe	Asp	Lys	Leu	Tyr	Lys	Ser	Leu
			340					345					350		
Met	Phe	Gly	Phe	Thr	Glu	Thr	Asn	Ile	Ala	Glu	Asn	Tyr	Lys	Ile	Lys
	355					360						365			
Thr	Arg	Ala	Ser	Tyr	Phe	Ser	Asp	Ser	Leu	Pro	Pro	Val	Lys	Ile	Lys
	370					375					380				
Asn	Leu	Leu	Asp	Asn	Glu	Ile	Tyr	Thr	Ile	Glu	Glu	Gly	Phe	Asn	Ile
385				390						395					400
Ser	Asp	Lys	Asp	Met	Glu	Lys	Glu	Tyr	Arg	Gly	Gln	Asn	Lys	Ala	Ile
			405					410						415	
Asn	Lys	Gln	Ala	Tyr	Glu	Glu	Ile	Ser	Lys	Glu	His	Leu	Ala	Val	Tyr
		420						425				430			
Lys	Ile	Gln	Met	Cys	Lys	Ser	Val	Lys	Ala	Pro	Gly	Ile	Cys	Ile	Asp
	435					440					445				
Val	Asp	Asn	Glu	Asp	Leu	Phe	Phe	Ile	Ala	Asp	Lys	Asn	Ser	Phe	Ser
	450					455					460				
Asp	Asp	Leu	Ser	Lys	Asn	Glu	Arg	Ile	Glu	Tyr	Asn	Thr	Gln	Ser	Asn
465				470						475					480
Tyr	Ile	Glu	Asn	Asp	Phe	Pro	Ile	Asn	Glu	Leu	Ile	Leu	Asp	Thr	Asp
			485					490					495		
Leu	Ile	Ser	Lys	Ile	Glu	Leu	Pro	Ser	Glu	Asn	Thr	Glu	Ser	Leu	Thr
		500						505				510			
Asp	Phe	Asn	Val	Asp	Val	Pro	Val	Tyr	Glu	Lys	Gln	Pro	Ala	Ile	Lys
	515					520						525			
Lys	Ile	Phe	Thr	Asp	Glu	Asn	Thr	Ile	Phe	Gln	Tyr	Leu	Tyr	Ser	Gln
	530					535					540				
Thr	Phe	Pro	Leu	Asp	Ile	Arg	Asp	Ile	Ser	Leu	Thr	Ser	Ser	Phe	Asp
545				550						555					560
Asp	Ala	Leu	Leu	Phe	Ser	Asn	Lys	Val	Tyr	Ser	Phe	Phe	Ser	Met	Asp
			565					570					575		
Tyr	Ile	Lys	Thr	Ala	Asn	Lys	Val	Val	Glu	Ala	Gly	Leu	Phe	Ala	Gly
	580							585				590			
Trp	Val	Lys	Gln	Ile	Val	Asn	Asp	Phe	Val	Ile	Glu	Ala	Asn	Lys	Ser
	595					600						605			
Asn	Thr	Met	Asp	Lys	Ile	Ala	Asp	Ile	Ser	Leu	Ile	Val	Pro	Tyr	Ile
	610					615					620				
Gly	Leu	Ala	Leu	Asn	Val	Gly	Asn	Glu	Thr	Ala	Lys	Gly	Asn	Phe	Glu
625				630						635					640
Asn	Ala	Phe	Glu	Ile	Ala	Gly	Ala	Ser	Ile	Leu	Leu	Glu	Phe	Ile	Pro
			645					650					655		
Glu	Leu	Leu	Ile	Pro	Val	Val	Gly	Ala	Phe	Leu	Leu	Glu	Ser	Tyr	Ile
		660					665					670			
Asp	Asn	Lys	Asn	Lys	Ile	Ile	Lys	Thr	Ile	Asp	Asn	Ala	Leu	Thr	Lys
	675						680				685				
Arg	Asn	Glu	Lys	Trp	Ser	Asp	Met	Tyr	Gly	Leu	Ile	Val	Ala	Gln	Trp
	690					695					700				
Leu	Ser	Thr	Val	Asn	Thr	Gln	Phe	Tyr	Thr	Ile	Lys	Glu	Gly	Met	Tyr
705				710						715					720
Lys	Ala	Leu	Asn	Tyr	Gln	Ala	Gln	Ala	Leu	Glu	Glu	Ile	Ile	Lys	Tyr
			725					730					735		
Arg	Tyr	Asn	Ile	Tyr	Ser	Glu	Lys	Glu	Lys	Ser	Asn	Ile	Asn	Ile	Asp

740							745					750				
Phe	Asn	Asp	Ile	Asn	Ser	Lys	Leu	Asn	Glu	Gly	Ile	Asn	Gln	Ala	Ile	
		755					760					765				
Asp	Asn	Ile	Asn	Asn	Phe	Ile	Asn	Gly	Cys	Ser	Val	Ser	Tyr	Leu	Met	
	770					775					780					
Lys	Lys	Met	Ile	Pro	Leu	Ala	Val	Glu	Lys	Leu	Leu	Asp	Phe	Asp	Asn	
785					790					795					800	
Thr	Leu	Lys	Lys	Asn	Leu	Leu	Asn	Tyr	Ile	Asp	Glu	Asn	Lys	Leu	Tyr	
				805					810					815		
Leu	Ile	Gly	Ser	Ala	Glu	Tyr	Glu	Lys	Ser	Lys	Val	Asn	Lys	Tyr	Leu	
			820					825					830			
Lys	Thr	Ile	Met	Pro	Phe	Asp	Leu	Ser	Ile	Tyr	Thr	Asn	Asp	Thr	Ile	
		835					840					845				
Leu	Ile	Glu	Met	Phe	Asn	Lys	Tyr	Asn	Ser	Glu	Ile	Leu	Asn	Asn	Ile	
	850					855					860					
Ile	Leu	Asn	Leu	Arg	Tyr	Lys	Asp	Asn	Asn	Leu	Ile	Asp	Leu	Ser	Gly	
865					870					875					880	
Tyr	Gly	Ala	Lys	Val	Glu	Val	Tyr	Asp	Gly	Val	Glu	Leu	Asn	Asp	Lys	
				885					890					895		
Asn	Gln	Phe	Lys	Leu	Thr	Ser	Ser	Ala	Asn	Ser	Lys	Ile	Arg	Val	Thr	
			900					905					910			
Gln	Asn	Gln	Asn	Ile	Ile	Phe	Asn	Ser	Val	Phe	Leu	Asp	Phe	Ser	Val	
		915					920					925				
Ser	Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Lys	Asn	Asp	Gly	Ile	Gln	Asn	
	930					935					940					
Tyr	Ile	His	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Lys	Asn	Asn	Ser	
945					950					955					960	
Gly	Trp	Lys	Ile	Ser	Ile	Arg	Gly	Asn	Arg	Ile	Ile	Trp	Thr	Leu	Ile	
				965					970					975		
Asp	Ile	Asn	Gly	Lys	Thr	Lys	Ser	Val	Phe	Phe	Glu	Tyr	Asn	Ile	Arg	
			980					985					990			
Glu	Asp	Ile	Ser	Glu	Tyr	Ile	Asn	Arg	Trp	Phe	Phe	Val	Thr	Ile	Thr	
		995					1000					1005				
Asn	Asn	Leu	Asn	Asn	Ala	Lys	Ile	Tyr	Ile	Asn	Gly	Lys	Leu	Glu	Ser	
	1010					1015					1020					
Asn	Thr	Asp	Ile	Lys	Asp	Ile	Arg	Glu	Val	Ile	Ala	Asn	Gly	Glu	Ile	
1025					1030					1035					1040	
Ile	Phe	Lys	Leu	Asp	Gly	Asp	Ile	Asp	Arg	Thr	Gln	Phe	Ile	Trp	Met	
				1045					1050					1055		
Lys	Tyr	Phe	Ser	Ile	Phe	Asn	Thr	Glu	Leu	Ser	Gln	Ser	Asn	Ile	Glu	
			1060					1065					1070			
Glu	Arg	Tyr	Lys	Ile	Gln	Ser	Tyr	Ser	Glu	Tyr	Leu	Lys	Asp	Phe	Trp	
		1075					1080					1085				
Gly	Asn	Pro	Leu	Met	Tyr	Asn	Lys	Glu	Tyr	Tyr	Met	Phe	Asn	Ala	Gly	
	1090															

Ser	Asp	Glu	Phe	Tyr	Asn	Thr	Ile	Gln	Ile	Lys	Glu	Tyr	Asp	Glu	Gln
				1205						1210					1215
Pro	Thr	Tyr	Ser	Cys	Gln	Leu	Leu	Phe	Lys	Lys	Asp	Glu	Glu	Ser	Thr
			1220						1225					1230	
Asp	Glu	Ile	Gly	Leu	Ile	Gly	Ile	His	Arg	Phe	Tyr	Glu	Ser	Gly	Ile
			1235					1240						1245	
Val	Phe	Glu	Glu	Tyr	Lys	Asp	Tyr	Phe	Cys	Ile	Ser	Lys	Trp	Tyr	Leu
			1250					1255				1260			
Lys	Glu	Val	Lys	Arg	Lys	Pro	Tyr	Asn	Leu	Lys	Leu	Gly	Cys	Asn	Trp
			1265			1270				1275					1280
Gln	Phe	Ile	Pro	Lys	Asp	Glu	Gly	Trp	Thr	Glu					
				1285					1290						